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(54) Title: MEMBERS OF THE FC RECEPTOR HOMOLOG GENE FAMILY (FCRH1-3, 6), RELATED REAGENTS, AND USES THEREOF

(57) Abstract: The invention relates to members of the Fc receptor homolog (FcRH) subfamily, as well as fragments and variants thereof. Each FcRH is a Type I transmembrane receptor, preferably, comprises an extracellular region, a transmembrane region, and a cytoplasmic region. The cytoplasmic region preferably comprises one or more immunoreceptor tyrosine-based inhibitory or activation motifs ("ITIMs" or "ITAMs"). The invention provides polypeptides, nucleic acids, vectors, expression systems, and antibodies and antibody fragments related to the FcRHs as well as uses thereof. Such uses include uses in the diagnosis and treatment of a malignancy of hematopoietic cell lineage or an inflammatory or autoimmune disease in a subject and in the modulation of a humoral immune response in a subject.



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**MEMBERS OF THE FC RECEPTOR HOMOLOG GENE FAMILY
(FCRH1-3, 6), RELATED REAGENTS, AND USES THEREOF**

This application claims the benefit of U.S. Provisional Application No.
5 60/367,667, filed March 25, 2002.

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AI39816 awarded by NIAID. The government has certain rights in the invention.
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FIELD OF THE INVENTION

This invention relates generally to immunology and modulation of immunologic
responses in the context of inflammatory diseases and cancer.

BACKGROUND OF THE INVENTION
15

Receptors for the Fc region (FcRs) of Igs have broad tissue distribution patterns
and can modulate cellular and humoral immunity by linking their antibody ligands with
effector cells of the immune system (Ravetch, J. V. & Kinet, J.-P. (1991) *Annu. Rev.*
Immunol. 9, 457-492; Daeron, M. (1997) *Annu. Rev. Immunol.* 15, 203-234. These
20 cellular receptors have the ability to sense humoral concentrations of antibody, initiate
cellular responses in host defense, and participate in autoimmune disorders (Ravetch, J.
V. & Bolland, S. (2001) *Annu. Rev. Immunol.* 19, 275-290). Their diverse regulatory
roles depend on the Ig isotype specificity and cellular distribution of the individual FcR.
These Ig superfamily members share similarities in their ligand binding subunits, and
25 they may have inhibitory or activating signaling motifs in their intracellular domains or
instead pair with signal transducing subunits possessing activating signaling motifs.

Recently, characterization of FcR homologs in mice, the paired
Ig-like receptors (Kubagawa, H. et al. (1997) *Proc. Natl. Acad. Sci. USA* 94, 5261-
5266; Hayami, K. et al. (1997) *J. Biol. Chem.* 272, 7320-7327), and their relatives in
30 humans the Ig-like transcripts/ leucocyte Ig-like receptors (Borges, L. et al. (1997) *J.*
Immunol. 159, 5192-5196; Samaridis, J. & Colonna, M. (1997) *Eur. J. Immunol.* 27,
660-665) have been elucidated. This multigene family, which includes the FcαR
(Kremer, E. J. et al. (1992) *Hum. Genet.* 89, 107-108) and the natural killer cell Ig-like

receptors (Wagtmann, N. et al. (1997) *Curr. Biol.* 7, 615-618), is located in a human chromosome 19q13 region known as the leucocyte receptor complex (LRC) (Wende, H. et al. (1999) *Mamm. Genome* 10, 154-160; Wilson, M. J. et al. (2000) *Proc. Natl. Acad. Sci. USA* 97, 4778-4783). These Ig-like multigene families belong to a larger class of

5 receptors characterized by their possession of common cytoplasmic tyrosine-based signaling motifs. These can be either immunoreceptor tyrosine-based activation motifs (ITAMs) containing two repeats of the consensus sequence Y-X-X-L/I spaced by 6-8 amino acids (E/D)-X-X-Y-X-X-(L/I)-X₆₋₈-Y-X-X-(L/I) (SEQ ID NO:64, with six amino acid between the consensus sequences; SEQ ID NO:65, with seven amino acid residues

10 between the consensus sequences; and SEQ ID NO:66, with eight amino acid residues between the consensus sequences) or immunoreceptor tyrosine-based inhibitory motifs (ITIMs) with a 6-amino acid consensus sequence (I/V/L/S)-X-Y-X-X-(L/V) (SEQ ID NO:67) (Reth, M. (1992) *Annu. Rev. Immunol.* 10, 97-121; Vely, F. & Vivier, E. (1997) *J. Immunol.* 159, 2075-2077; Ravetch, J. V. & Lanier, L. L. (2000) *Science* 290,

15 84-89; Gergely, J. et al. (1999) *Immunol. Lett.* 68, 3-15). The phylogenetic conservation of these types of receptors in birds (Dennis, G. et al. (2000) *Proc. Natl. Acad. Sci. USA* 97, 13245-13250) and bony fish (Yoder, J. A. et al. (2001) *Proc. Natl. Acad. Sci. USA* 98, 6771-6717) is indicative of their biological value. After ligand binding of the activating receptor complexes, ITAM tyrosines are rapidly phosphorylated by Src

20 family kinases to initiate a cascade of signaling events that trigger cellular activation. In the case of ITIM-bearing receptors, the tyrosines provide a docking site for phosphatases containing Src homology 2 domains that can abrogate cellular activation (Long, E. O. (1999) *Annu. Rev. Immunol.* 17, 875-904; Unkeless, J. C. & Jin, J. (1997) *Curr. Opin. Immunol.* 9, 338-343). The balance in the utilization of these activating and

25 inhibitory receptor pairs can serve to modulate cellular responses to a variety of stimuli.

The genes encoding the classical FcγRs, FcγRI, FcγRII, FcγRIII, and FcεRI, lie on the long arm of chromosome 1 (1q21-23) near the polymeric Ig receptor (pIgR) and Fcα/μR genes (1q32) (20-23). Members of this FcR subfamily have relatively low extracellular homology with the FcR-related genes that reside in the LRC on

30 chromosome 19. Like the FcγR- and FcεR-activating receptors, the ligand binding chain of the FcαR coassociates with the ITAM containing FcR common γ-chain

(Pfefferkorn, L. C. & Yeaman, G. R. (1994) J. Immunol. 153, 3228-3236; Morton, E. C. et al. (1995) J. Biol. Chem. 270, 29781-29787). New members of the FcR family were sought which could have diverse signally properties and oncogenic potential.

5

SUMMARY OF THE INVENTION

In accordance with the purpose(s) of this invention, as embodied and broadly described herein, this invention, in one aspect, relates to members of a cluster of FcR and FcR gene relatives encoded, for example, by genes in the human chromosome 1q21-23 region, or analogous region in non-human subjects. The members are Type I
10 transmembrane receptors, or alternatively spliced forms thereof, with homology to the FcR family and are referred to herein as FcRHs. Each FcRH can comprise an extracellular region, a transmembrane region, and a cytoplasmic region. The cytoplasmic region preferably comprises one or more immunoreceptor tyrosine-based inhibitory or activation motifs ("ITIMs" or "ITAMs").

15

The invention relates to polypeptides corresponding to isolated FcRHs (e.g., huFcRH 1, 2, 3, and 6 and moFcRH1, 2, and 3), as well as fragments and isoforms thereof. The invention further relates to nucleic acids that encode the FcRHs, as well as hybridization probes related thereto and complementary sequences. The invention further provides vectors and cells related to the nucleic acids of the invention.

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The invention further relates to making an FcRH, or a fragment or variant thereof, comprising culturing a cell comprising a vector of the invention under conditions permitting expression of the FcRH. The invention also provides an antibody reagent kit comprising the antibody, or a fragment or variant thereof, and reagents for detecting binding of the antibody, fragment, or antibody variant to a ligand.

25

The invention further relates to uses of the polypeptides, nucleic acids and antibodies of the invention. For example, the invention relates to methods of diagnosing and methods of treating a malignancy of hematopoietic cell lineage or an inflammatory or autoimmune disease in a subject. The invention also relates to modulation of a humoral immune response in a subject.

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Additional advantages of the invention will be set forth in part in the description which follows, and in part will be obvious from the description, or may be learned by practice of the invention. The advantages of the invention will be realized and attained by means of the elements and combinations particularly pointed out in the appended

claims. It is to be understood that both the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of the invention, as claimed.

5

BRIEF DESCRIPTION OF THE DRAWINGS

The accompanying drawings, which are incorporated in and constitute a part of this specification, illustrate (one) several embodiment(s) of the invention and together with the description, serve to explain the principles of the invention.

Figure 1 shows the relative position of the FcRH locus within the FcR cluster on chromosome 1. The cytogenetic location of the FcR genes is approximated from the GenBank Mapview database. The BAC clones (4, GenBank accession no. AL139409; 3, GenBank accession no. AL356276; 2, GenBank accession no. AL135929; and 1, GenBank accession no. AL353721) that span the locus are oriented in relation to their respective FcRH genes (shaded area).

15

Figure 2 shows the structural and sequence diversity of FcRH1, FcRH2, and FcRH3. Figure 2A is a schematic representation of FcRH molecules. The three cDNAs encode type I transmembrane proteins with similar extracellular domains, but different cytoplasmic regions. The extracellular (EC) regions contain different numbers of C2-like Ig domains and potential sites of N-linked glycosylation. The transmembrane (TM) domains are uncharged, except in the case of FcRH1. The cytoplasmic (CY) region of FcRH1 contains two ITAMs (light gray boxes) and one ITAM-like region (small, lined box), whereas FcRH2 contains one ITAM and two ITIMs (dark gray boxes). FcRH3 has a long cytoplasmic tail with one ITAM, one ITIM, and an ITAM-like region. The amino acid length of each region is indicated. Figure 2B shows the multiple alignment comparison of FcRH1, FcRH2, and FcRH3 amino acid sequences (one-letter code) based on the FcRH3 sequence. Amino acid identity is represented by dots, and gaps are indicated by dashes. Predicted N-linked glycosylation sites and transmembrane domains are underlined in black. Consensus ITAM (bold) and ITIM (bold, underlined) motifs are indicated. Putative structural domains are labeled: SP, signal peptide; EC, extracellular domain; MP-TM, membrane proximal-transmembrane; and CY, cytoplasmic regions. Amino acid lengths are indicated in parentheses.

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Figure 3 shows a composite analysis of the extracellular homology among FcRH and FcR family members. Pairwise analysis of individual Ig-like subunits was

performed with the CLUSTAL method algorithm using FcRH3 as the index of comparison. Individual homologous domains are coded to indicate relatedness. Percent amino acid identities for related domains are indicated and aligned in relation to the comparative FcRH3 subunit. The amino acid identity for the membrane proximal domains (light gray subunits) of FcRH5 are provided as the range of identity for all individually related domains. Comparisons that are not applicable are left blank. Amino acid sequences were derived from IRTA1 (GenBank accession no. AF343659), IRTA2 (GenBank accession no. AF34364), moFcRH (GenBank accession no. AAG28775) FcγRI (GenBank accession no. AAA35678), FcγRII (Swiss-Prot accession no. P31994), FcγRIII (Swiss-Prot accession no. P08637), FcεRI (Swiss-Prot accession no. P12319), and FcαRI (Swiss-Prot accession no. P24071).

Figure 4 shows the relative location of the mouse FcR family. Location is indicated in reference to the human FcR related genes at Ch 1q21-23 and their orthologous loci on mouse Ch 3 and Ch 1. The microsatellite marker d3Mit187 is located within moFcRH1.

Figure 5 shows the multiple alignment comparisons of huFcRH1-5 and mouse FcRH1 and 2 amino acid sequences (one-letter code) based on the FcRH3 sequence. Amino acid gaps are indicated by dashes. Consensus ITAM (underlined) and ITIM (italic, underlined) motifs are indicated. Amino acid lengths are indicated in parentheses.

Figure 6 shows domains marked to indicate relatedness of the Ig-like subunits. Ig-like domain homology was determined by generation of a phylogenetic tree using DNASTar software with the CLUSTAL program and assigning arbitrary colors to individual Ig-domains of a given branch. Amino acid identities for full length, extracellular and, cytoplasmic domain comparisons are based on huFcRH3. Closest cytoplasmic relatives are indicated in parentheses. Most identical extracellular comparisons between mouse and human relatives are highlighted in horizontal lines. Comparisons that are not applicable are left blank.

Figure 7 shows the domains of huFcRH1-6, moFcRH1-3 and related proteins. Domains are colored to indicate relatedness of the Ig-like subunits. Ig-like domain homology was determined by generation of a phylogenetic tree using DNASTar software with the CLUSTAL program and assigning arbitrary colors to individual Ig-domains of a given branch. Amino acid identities for full length, extracellular and, cytoplasmic

domain comparisons are based on huFcRH3. Closest cytoplasmic relatives are indicated in parentheses. Most identical extracellular comparisons between mouse and human relatives are highlighted in red. Comparisons that are not applicable are left blank.

Figure 8 shows the structural characteristics of the mouse FcRH isoforms.

5

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention may be understood more readily by reference to the following detailed description of preferred embodiments of the invention and the Examples included therein and to the Figures and their previous and following description.

10

In this specification and in the claims that follow, reference will be made to a number of terms that shall be defined to have the following meanings:

As used in the specification and the appended claims, the singular forms “a,” “an” and “the” include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to a receptor includes mixtures of various receptors, reference to “a pharmaceutical carrier” includes mixtures of two or more such carriers, and the like.

15

Ranges may be expressed herein as from “about” one particular value, and/or to “about” another particular value. When such a range is expressed, another embodiment includes from the one particular value and/or to the other particular value. Similarly, when values are expressed as approximations, by use of the antecedent “about,” it will be understood that the particular value forms another embodiment. It will be further understood that the endpoints of each of the ranges are significant both in relation to the other endpoint, and independently of the other endpoint.

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“Optional” or “optionally” means that the subsequently described event or circumstance may or may not occur, and that the description includes instances where said event or circumstance occurs and instances where it does not. For example, the phrase “optionally contains two ITAM consensus motifs” means that the two ITAMs may or may not be present and that the description includes both the presence and absence of two ITAM consensus motifs.

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As used throughout, by “subject” is meant an individual. Preferably, the subject is a mammal such as a primate, and, more preferably, a human. The term “subject” can

include domesticated animals, such as cats, dogs, etc., livestock (e.g., cattle, horses, pigs, sheep, goats, etc.), and laboratory animals (e.g., mouse, rabbit, rat, guinea pig, etc.).

By "isolated nucleic acid" is meant a nucleic acid the structure of which is not identical to that of the naturally occurring nucleic acid or to that of any fragment of the naturally occurring genomic nucleic acid spanning more than three separate genes. The term therefore covers, for example, (a) a DNA which has the sequence of part of the naturally occurring genomic DNA molecules but is not flanked by both of the coding sequences that flank that part of the molecule in the genome of the organism in which it naturally occurs; (b) a nucleic acid incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA; (c) a separate molecule such as cDNA, a genomic fragment, a fragment produced by polymerase chain reaction, or a restriction fragment; and (d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion protein.

By "label" is meant any detectable tag that can be attached directly (e.g., a fluorescent molecule integrated into a polypeptide or nucleic acid) or indirectly (e.g., by way of binding to a primary antibody a secondary antibody with an integrated fluorescent molecule) to the molecule of interest. A "label" is any tag that can be visualized with imaging methods. The detectable tag can be a radio-opaque substance, radiolabel, a fluorescent label, or a magnetic label. The detectable tag can be selected from the group consisting of gamma-emitters, beta-emitters, and alpha-emitters, gamma-emitters, positron-emitters, X-ray-emitters and fluorescence-emitters suitable for localization. Suitable fluorescent compounds include fluorescein sodium, fluorescein isothiocyanate, phycoerythrin, and Texas Red sulfonyl chloride. See, de Belder & Wik (Preparation and properties of fluorescein-labelled hyaluronate. Carbohydr. Res.44(2):251-57 (1975). Those skilled in the art will know, or will be able to ascertain with no more than routine experimentation, other fluorescent compounds that are suitable for labeling the molecule.

Polypeptides

The invention provides members of a cluster of FcR and FcR gene relatives encoded by genes in the human chromosome 1q21-23 region, or analogous region in non-human subjects, including for example, chromosome 3 in mouse. A consensus amino acid motif, based on the FcγRI, FcγRII, FcγRIII, and pIgR extracellular regions,

was used in a GenBank protein database query to identify member of the gene subfamily. Genomic clones were identified that were found to contain FcR relatives and are termed the Fc receptor homolog (FcRH) subfamily: specifically, FcRH1, FcRH2, FcRH3, and FcRH6. Also, found were mouse Fc receptor homologs

5 designated moFcR1, 2, and 3.

By "homologous" is meant about 25% percent homology or greater. Homology is also characterized by proximity in the location of the genes and by similarities as identified in a composite analysis. As used herein, "percent homology" of two amino acid sequences or of two nucleic acid sequences is determined using the algorithm of

10 Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87:2264-2268 (1990)). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (J. Mol. Biol. 215:403-410 (1990)). BLAST nucleotide searches are performed with the NBLAST program, score 100, wordlength = 12, to obtain nucleotide sequences homologous to a nucleic acid molecule of the invention. BLAST protein searches are

15 performed with the XBLAST program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to a reference polypeptide. To obtain gapped alignments for comparison purposes, Gapped Blast is utilized as described in Altschul et al. (Nucl. Acids Res. 25: 3389-3402 (1997)). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and

20 NBLAST) are used. See <http://www.ncbi.nlm.nih.gov>.

By "FcRH" is meant a Type I transmembrane receptor, or an alternatively spliced form thereof, including, for example, a secreted form or a GPI-anchored form, with homology to the classical Fc receptor family. In a preferred embodiment, the FcRH shows homology with the extracellular regions of FcγRI, FcγRII, FcγRIII, or

25 pIgR. More specifically, the FcRH shows homology with an amino acid sequence corresponding with the amino terminal sequences of the second Ig domains of the FcγRs and the third Ig domain of pIgR or FcγRH1. The FcRH can comprise an extracellular region, a transmembrane region, and a cytoplasmic region. The extracellular region preferably comprises one or more Ig domains, and more preferably

30 less than 9, and even more preferably less than 7 or less than 8 Ig domains. Preferably, the cytoplasmic region comprises more than 107 (including more than 108, 109, 110, 111, 112, 113, 114, 115, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, or 145 amino acids).

Alternatively, the cytoplasmic region comprises less than 104 amino acids (including less than 103, 102, 101, 100, 99, 98, 97, 96, 95, 94, 93, 92, 91, 90, 89, 88, 87, 86, 85, 84, 83, 82, 81, 80). The cytoplasmic region preferably comprises one or more immunoreceptor tyrosine-based inhibitory or activation motifs ("ITIMs" or "ITAMs).

5 The invention provides isolated FcRHs (e.g., huFcRH 1, 2, 3, and 6, and moFcRH1-3, as described in detail below), as well as fragments and isoforms thereof. The isolated amino acid sequences provided herein optionally are combined with a human signal sequence (e.g., MLPRLLLLICAPLCEP (SEQ ID NO:29), MLLWSLLVIFDAVTEQADS (SEQ ID NO:30), MLLWLLLLLTPGREQS (SEQ ID NO:31), MLLWTAVLLFVPCVG (SEQ ID NO:32)) or a mouse signal sequence (e.g., MPLCLLLLVFAPVGVQS (SEQ ID NO:69), MLPWLLLLLICALPCEPA (SEQ ID NO:72), MSGSFSPCVVFTQMWLTLLVVTPVN (SEQ ID NO:79)).

15 In one embodiment, the invention provides huFcRH1 and its fragments and isoforms. Thus, in one embodiment of the isolated FcRH, the extracellular region comprises less than four Ig domains. Preferably, the cytoplasmic region comprises less than 104 amino acids and, even more preferably, comprises less than 104 and more than 86 amino acids. In one embodiment, the transmembrane region comprises an acidic amino acid (e.g., glutamate or aspartate). The isolated FcRH of the invention comprises a cytoplasmic region having the amino acid sequence of SEQ ID NO:1, in the presence or absence of conservative amino acid substitutions. Further provided is the isolated FcRH, wherein the extracellular region comprises the amino acid sequence of SEQ ID NO:21, in the presence or absence of conservative amino acid substitutions, and in the presence and absence of a signal sequence. More specifically, the isolated FcRH comprises the amino acid sequence of SEQ ID NO:2, in the presence or absence of conservative amino acid substitutions, and in the presence or absence of a signal sequence. In one embodiment the signal sequence is MLPRLLLLICAPLCEP (SEQ ID NO:29). In a preferred embodiment, the FcRH of the invention is expressed by myeloid cells (e.g., granulocytes and monocytes). Additional characteristics of the full length FcRH1 include a predicted molecular weight of about 46-47 kDaltons; about 425-435 (e.g., 429) amino acids in length with about 35 strongly basic(+) amino acids (K,R), about 45 strongly acidic(-) amino acids (D,E), about 144 hydrophobic amino acids (A,I,L,F,W,V), and about 127 polar amino acids (N,C,Q,S,T,Y); a predicted isoelectric point of about 5-5.5 (e.g., 5.310); and charge of about -9 at PH 7.0.

In another embodiment, the invention provides an isolated FcRH corresponding to huFcRH2, its fragments, or isoforms. Thus, the invention provides a FcRH wherein the cytoplasmic region comprises less than 99 amino acids (e.g., 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98) and wherein the receptor further comprises an extracellular domain with up to four Ig domains and up to five N-linked glycosylation sites. More specifically, the isolated FcRH has a cytoplasmic region that comprises the amino acid sequence of SEQ ID NO:3, in the presence or absence of conservative amino acid substitutions, or an extracellular region comprising SEQ ID NO:22, in the presence or absence of conservative amino acid substitutions, and in the presence or absence of a signal sequence. Even more specifically, the isolated FcRH comprises the amino acid sequence of SEQ ID NO:4, in the presence or absence of conservative amino acid substitutions, and in the presence or absence of a signal sequence. In one embodiment, the signal sequence WSLLVIFDAVTEQADS (SEQ ID NO:30). Additional characteristics of the full length FcRH1 include a predicted molecular weight of about 50-60 kDaltons; about 495-515 (e.g., 508) amino acids in length with about 44 strongly basic(+) amino acids (K,R), about 49 strongly acidic(-) amino acids (D,E), about 175 hydrophobic amino acids (A,I,L,F,W,V), and about 161 polar amino acids (N,C,Q,S,T,Y); a predicted isoelectric point of about 6-6.5 (e.g., 6.188); and charge of about -4 at PH 7.0.

In another embodiment, the invention provides huFcRH3, its fragments, and isoforms. More specifically, the invention provides an isolated FcRH having a cytoplasmic region that comprises more than 107 amino acids (e.g., 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150 amino acids). Optionally, the isolated FcRH has a cytoplasmic region comprising one ITAM and one ITIM. More specifically, the cytoplasmic region comprises the amino acid sequence of SEQ ID NO:5 or SEQ ID NO:23, in the presence or absence of conservative amino acid substitutions. In one embodiment, the extracellular domain of the FcRH comprises the amino acid sequence of SEQ ID NO:24, in the presence or absence of conservative amino acid substitutions, and in the presence or absence of a signal sequence. Also provided is an isolated FcRH comprising the amino acid sequence of SEQ ID NO:6 or SEQ ID NO:25, in the presence or absence of one or more amino acid substitutions, and in the presence or

absence of a signal sequence. In one embodiment the signal sequence comprises MLLWLLLLLTPGREQS (SEQ ID NO:31). Additional characteristics of the full length FcRH1 include a predicted molecular weight of about 80-90 kDaltons; about 725-740 (e.g., 734) amino acids in length with about 68 strongly basic(+) amino acids (K,R), about 75 strongly acidic(-) amino acids (D,E), about 232 hydrophobic amino acids (A,I,L,F,W,V), and about 224 polar amino acids (N,C,Q,S,T,Y); a predicted isoelectric point of about 6.5-7.0 (e.g., 6.852); and charge of about -2 at PH 7.0.

The invention further provides an isolated huFcRH6, its fragments, and isoforms. More specifically, the FcRH comprises a cytoplasmic region having the amino acid sequence of SEQ ID NO:26, in the presence or absence of one or more conservative amino acid substitutions. The extracellular domain comprises the amino acid sequence of SEQ ID NO:27, in the presence or absence of conservative amino acid substitutions, and in the presence or absence of a signal sequence. Also, provided by the invention is a FcRH having the amino acid substitutions of SEQ ID NO:28, in the presence or absence of conservative amino acid substitutions, and in the presence or absence of a signal sequence. In one embodiment the signal sequence is MLLWTAVLLFVPCVG (SEQ ID NO:32).

The invention further provides a polypeptide comprising the amino acid sequence of SEQ ID NO:1, 21, 2, 3, 22, 4, 5, 23, 24, 6, 25, 26, 27, or 28, in the presence or absence of conservative amino acid substitutions. The invention also provides a polypeptide having at least 80, 85, 90, or 95% homology with SEQ ID NOs: 1, 21, 2, 3, 22, 4, 5, 23, 24, 6, 25, 26, 27, or 28.

The invention further provides an isolated moFcRH1 isoform, its fragments, and isoforms. The moFcRH1 is an isoform of SEQ ID NO:68. More specifically, the FcRH comprises four Ig domains, optionally having the sequence of SEQ ID NO: 70, in the presence or absence of one or more conservative amino acid substitutions, and in the presence or absence of a signal sequence (e.g., the sequence of SEQ ID NO:71).

The invention further provides an isolated moFcRH2, its fragments, and isoforms. The provided isoforms include one isoform with a transmembrane region and one isoform lacking the transmembrane region. More specifically, the FcRH comprises a cytoplasmic region having the amino acid sequence of SEQ ID NO:76, in the presence or absence of one or more conservative amino acid substitutions. The extracellular domain comprises the amino acid sequence of SEQ ID NO:74, in the presence or

absence of conservative amino acid substitutions, and in the presence or absence of a signal sequence. Also, provided by the invention is a FcRH having the amino acid sequence of SEQ ID NO:73, which comprises a transmembrane region, or SEQ ID NO:77, which lacks the transmembrane region. In each case, the FcRH sequence can
5 include the presence or absence of conservative amino acid substitutions, and the presence or absence of a signal sequence. In one embodiment the signal sequence is the sequence of SEQ ID NO:72.

The invention also provided a moFcRH3, its fragments and isoforms. The cytoplasmic region can comprise the amino acid sequence of SEQ ID NO:81, in the
10 presence or absence of conservative amino acid substitutions. Optionally, the extracellular domain comprises the amino acid sequence of SEQ ID NO:80, in the presence or absence of conservative amino acid substitutions or in the presence or absence of a signal sequence (e.g., the sequence of SEQ ID NO:79). The full length sequence optionally has the amino acid sequence of SEQ ID NO:78, in the presence or
15 absence of conservative amino acid substitutions or in the presence or absence of a signal sequence (e.g., the sequence of SEQ ID NO:79).

Fragments, variants, or isoforms of the FcRHs of the invention are provided. It is understood that these terms include functional variants. Fragments can include the cytoplasmic region, the extracellular region, the transmembrane region or any portion of
20 at least 10 amino acids or any combination of the regions or portions. The variants are produced by making amino acid substitutions, deletions, and insertions, as well as post-translational modifications. Variations in post-translational modifications can include variations in the type or amount of carbohydrate moieties of the protein core or any fragment or derivative thereof. Variations in amino acid sequence may arise naturally
25 as allelic variations (e.g., due to genetic polymorphism) or may be produced by human intervention (e.g., by mutagenesis of cloned DNA sequences), such as induced point, deletion, insertion and substitution mutants. These modifications can result in changes in the amino acid sequence, provide silent mutations, modify a restriction site, or provide other specific mutations.

30 Amino acid sequence modifications fall into one or more of three classes: substitutional, insertional or deletional variants. Insertions include amino and/or carboxyl terminal fusions as well as intrasequence insertions of single or multiple amino acid residues. Insertions ordinarily will be smaller insertions than those of

amino or carboxyl terminal fusions, for example, on the order of one to four residues. Deletions are characterized by the removal of one or more amino acid residues from the protein sequence. Typically, no more than about 2 to 6 residues are deleted at any one site within the protein molecule. These variants ordinarily are prepared by site-specific mutagenesis of nucleotides in the DNA encoding the protein, thereby producing DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known and include, for example, M13 primer mutagenesis and PCR mutagenesis. Amino acid substitutions are typically of single residues but may include multiple substitutions at different positions; insertions usually will be on the order of about from 1 to 10 amino acid residues but can be more; and deletions will range about from 1 to 30 residues, but can be more. Deletions or insertions preferably are made in adjacent pairs, i.e. a deletion of 2 residues or insertion of 2 residues. Substitutions, deletions, insertions or any combination thereof may be combined to arrive at a final construct. The mutations must not place the sequence out of reading frame and preferably will not create complementary regions that could produce secondary mRNA structure. Substitutional variants are those in which at least one residue has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with Table 1 and are referred to as conservative substitutions.

| TABLE 1: | Amino Acid Substitutions |
|------------------|--------------------------|
| Original Residue | Exemplary Substitutions |
| Ala | Ser |
| Arg | Lys |
| Asn | Gln |
| Asp | Glu |
| Cys | Ser |
| Gln | Asn |
| Glu | Asp |
| Gly | Pro |
| His | Gln |
| Ile | Leu; Val |
| Leu | Ile; Val |
| Lys | Arg; Gln |
| Met | Leu; Ile |
| Phe | Met; Leu; Tyr |
| Ser | Thr |
| Thr | Ser |

| | |
|-----|----------|
| Trp | Tyr |
| Tyr | Trp; Phe |
| Val | Ile; Leu |

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those in Table 1, i.e., selecting residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site or (c) the bulk of the side chain. The substitutions that in general are expected to produce the greatest changes in the protein properties will be those in which (a) a hydrophilic residue, e.g. seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine, in this case, (e) by increasing the number of sites for sulfation and/or glycosylation.

Substitutional or deletional mutagenesis can be employed to insert sites for N-glycosylation (Asn-X-Thr/Ser) or O-glycosylation (Ser or Thr). Deletions of cysteine or other labile residues also may be desirable. Deletions or substitutions of potential proteolysis sites, e.g. Arg, is accomplished for example by deleting one of the basic residues or substituting one by glutaminyl or histidyl residues.

Certain post-translational derivatizations are the result of the action of recombinant host cells on the expressed polypeptide. Glutaminyl and asparaginyl residues are frequently post-translationally deamidated to the corresponding glutamyl and aspartyl residues. Alternatively, these residues are deamidated under mildly acidic conditions. Other post-translational modifications include hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the o-amino groups of lysine, arginine, and histidine side chains (T.E. Creighton, *Proteins: Structure and Molecular Properties*, W. H. Freeman & Co., San Francisco pp 79-86 [1983]), acetylation of the N-terminal amine and, in some instances, amidation of the C-terminal carboxyl. Modifications in the FcRH can also include modifications in glycosylation.

In all mutational events, it is understood that the controlling aspect of the mutation is the function that the subsequent protein possesses. The preferred mutations are those that do not detectably change the desired function or that increase the desired function.

5

Nucleic Acids

Also provided is an isolated nucleic acid that encodes the FcRH of the invention. The nucleic acid can be single or double stranded and can be RNA or DNA. More specifically, the invention provides an isolated nucleic acid, comprising a

10 nucleotide sequence that encodes SEQ ID NO:1, SEQ ID NO:21, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:22, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, or SEQ ID NO:6, SEQ ID NO:70, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:81, optionally with conservative

15 amino acid substitutions. Optionally the nucleic acid further encodes a signal sequence (e.g., the signal sequences of SEQ ID NO:29, 30, 31, 32, 71, 75, 79). The isolated nucleic acid optionally encodes the sequences with 80, 85, 90, or 95 % identity. More specifically, the invention provides an isolated nucleic acid, comprising a nucleotide

20 sequence of SEQ ID NO:7, SEQ ID NO:13, SEQ ID NO:8, SEQ ID NO:34, SEQ ID NO:9, SEQ ID NO:14, SEQ ID NO:10, SEQ ID NO:36, SEQ ID NO:11, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:12, SEQ ID NO:38, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20; SEQ ID NO:40, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID

25 NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, or SEQ ID NO:102. Optionally, the isolated nucleic acid can further include bases that encode a signal sequence and thus the nucleotide sequence encoding the extracellular region or full-length huFcRH1, 2, 3, or 6 can optionally further comprise the nucleotide sequence of SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID

30 NO:39. Optionally, the isolated nucleic acids for moFcRHs include nucleic acid sequences that encode signal sequences as well, including for example, those portions of nucleic acid sequences SEQ ID NO:101, SEQ ID NO:97, SEQ ID NO:94, SEQ ID NO:91, SEQ ID NO:88, SEQ ID NO:84.

Preferably the nucleic acid that encodes the full length FcRH1 includes about 1290 bases. The nucleic acid that encodes the full length FcRH2 includes about 1527 bases, and the nucleic acid that encodes the full length FcRH3 includes about 2205 bases.

5 The invention also provides an isolated nucleic acid comprising a sequence that hybridizes under stringent conditions to a hybridization probe, wherein the hybridization probe comprises the nucleotide sequence of SEQ ID NO:7, SEQ ID NO:13, SEQ ID NO:8, SEQ ID NO:34, SEQ ID NO:9, SEQ ID NO:14, SEQ ID NO:10, SEQ ID NO:36, SEQ ID NO:11, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:12, SEQ
10 ID NO:38, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, and SEQ ID NO:20; SEQ ID NO:40, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, or SEQ ID NO:102, or the complement of
15 either sequence.

Further provided is a single stranded nucleic acid that hybridizes under stringent conditions to a nucleic acid having the sequence of SEQ ID NO:7, SEQ ID NO:13, SEQ ID NO:8, SEQ ID NO:34, SEQ ID NO:9, SEQ ID NO:14, SEQ ID NO:10, SEQ ID NO:36, SEQ ID NO:11, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:12, SEQ ID
20 NO:38, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, and SEQ ID NO:20; SEQ ID NO:40, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, or SEQ ID NO:102.

25 By “hybridizing under stringent conditions” or “hybridizing under highly stringent conditions” is meant that the hybridizing portion of the hybridizing nucleic acid, typically comprising at least 15 (e.g., 20, 25, 30, or 50 nucleotides), hybridizes to all or a portion of the provided nucleotide sequence under stringent conditions. The term “hybridization” typically means a sequence driven interaction between at least two
30 nucleic acid molecules, such as a primer or a probe and a gene. Sequence driven interaction means an interaction that occurs between two nucleotides or nucleotide analogs or nucleotide derivatives in a nucleotide specific manner. For example, G interacting with C or A interacting with T are sequence driven interactions. Typically

sequence driven interactions occur on the Watson-Crick face or Hoogsteen face of the nucleotide. The hybridization of two nucleic acids is affected by a number of conditions and parameters known to those of skill in the art. For example, the salt concentrations, pH, and temperature of the reaction all affect whether two nucleic acid molecules will hybridize. Generally, the hybridizing portion of the hybridizing nucleic acid is at least 80%, for example, at least 90%, 95%, or 98%, identical to the sequence of or a portion of a nucleic acid encoding an FcRH of the invention, or its complement. Hybridizing nucleic acids of the invention can be used, for example, as a cloning probe, a primer (e.g., for PCR), a diagnostic probe, or an antisense probe.

Hybridization of the oligonucleotide probe to a nucleic acid sample typically is performed under stringent conditions. Nucleic acid duplex or hybrid stability is expressed as the melting temperature or T_m , which is the temperature at which a probe dissociates from a target DNA. This melting temperature is used to define the required stringency conditions. If sequences are to be identified that are related and substantially identical to the probe, rather than identical, then it is useful to first establish the lowest temperature at which only homologous hybridization occurs with a particular concentration of salt (e.g., SSC or SSPE). Assuming that a 1% mismatch results in a 1°C decrease in the T_m , the temperature of the final wash in the hybridization reaction is reduced accordingly (for example, if sequence having >95% identity with the probe are sought, the final wash temperature is decreased by 5°C). In practice, the change in T_m can be between 0.5°C and 1.5°C per 1% mismatch. Stringent conditions involve hybridizing at 68°C in 5x SSC/5x Denhardt's solution/1.0% SDS, and washing in 0.2x SSC/0.1% SDS at room temperature. Moderately stringent conditions include washing in 3x SSC at 42°C . The parameters of salt concentration and temperature can be varied to achieve the optimal level of identity between the probe and the target nucleic acid. Additional guidance regarding such conditions is readily available in the art, for example, in Sambrook et al., 1989, Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, NY; and Ausubel et al. (eds.), 1995, Current Protocols in Molecular Biology, (John Wiley & Sons, NY) at Unit 2.10.

The nucleic acids of the present invention are optionally labeled, directly or indirectly. Such labeled nucleic acids are useful in various diagnostic techniques including for example, *in situ* hybridization, FISH, *in situ* PCR, and PRINS. Both

methods involve the preparation of short sequences of single-stranded nucleic acid probes that are complementary to the nucleic acid sequences that encode an FcRH. See, e.g., M Andreeff and D Pinkel (1999), An Introduction to Fluorescent In-Situ Hybridization: Principles and Clinical Applications, John Wiley & Sons, Ltd; Roche Applied Sciences (2000), Nonradioactive In Situ Hybridization Application Manual; Roche Applied Sciences (1999), PCR Manual, 2d edition, which are incorporated in their entirety for methods of using nucleic acids.

Vectors, cells, and methods of using

Also provided is an expression vector comprising a nucleic acid of the invention, wherein the nucleic acid is operably linked to an expression control sequence. A wide variety of expression system/regulatory sequence combinations may be employed in expressing the disclosed. Such useful regulatory sequences include, for example, the early or late promoters of SV40, CMV, vaccinia, polyoma or adenovirus, the lac system, the trp system, the TAC system, the TRC system, the LTR system, the major operator and promoter regions of phage lambda, the control regions of fd coat protein, the promoter for 3-phosphoglycerate kinase or other glycolytic enzymes, the promoters of acid phosphatase (for example, Pho5), the AOX 1 promoter of methylotrophic yeast, the promoters of the yeast a-mating factors, and other sequences known to control the expression of genes of prokaryotic or eukaryotic cells or their viruses, and various combinations thereof.

Such an expression vector can be designed to be expressed by eukaryotic cells or prokaryotic cells. The vectors of the present invention thus provide DNA molecules which are capable of integration into a prokaryotic or eukaryotic chromosome and expression. The inserted genes in viral and retroviral vectors usually contain promoters, and/or enhancers to help control the expression of the desired gene product. A promoter is generally a sequence or sequences of DNA that function when in a relatively fixed location in regard to the transcription start site. A promoter contains core elements required for basic interaction of RNA polymerase and transcription factors, and may contain upstream elements and response elements. It has been shown that all specific regulatory elements can be cloned and used to construct expression vectors that are selectively expressed in specific cell types. For example, the glial fibrillary acidic protein (GFAP) promoter has been used to selectively express genes in

cells of glial origin. Expression vectors used in eukaryotic host cells (e.g., yeast, fungi, insect, plant, animal, human or nucleated cells) may also contain sequences necessary for the termination of transcription which may affect mRNA expression. These regions are transcribed as polyadenylated segments in the untranslated portion of the mRNA
5 encoding tissue factor protein. The 3' untranslated regions also include transcription termination sites. It is preferred that the transcription unit also contain a polyadenylation region. One benefit of this region is that it increases the likelihood that the transcribed unit will be processed and transported like mRNA. The identification and use of polyadenylation signals in expression constructs is well established. It is
10 preferred that homologous polyadenylation signals be used in the transgene constructs. In certain transcription units, the polyadenylation region is derived from the SV40 early polyadenylation signal and consists of about 400 bases. It is also preferred that the transcribed units contain other standard sequences alone or in combination with the above sequences improve expression from, or stability of, the construct.

15 The invention further provides transfer vectors, which include any nucleotide construction used to deliver genes into cells (e.g., a plasmid), or as part of a general strategy to deliver genes, e.g., as part of recombinant retrovirus or adenovirus (Ram et al. Cancer Res. 53:83-88, (1993)). As used herein, plasmid or viral vectors are agents that transport the disclosed nucleic acids into the cell without degradation and include a
20 promoter yielding expression of the gene in the cells into which it is delivered. In some embodiments the FcRHs are derived from either a virus or a retrovirus. Viral vectors include, for example, Adenovirus, Adeno-associated virus, Herpes virus, Vaccinia virus, Polio virus, AIDS virus, neuronal trophic virus, Sindbis and other RNA viruses, including these viruses with the HIV backbone. Also preferred are any viral families
25 that share the properties of these viruses that make them suitable for use as vectors. Retroviruses include Murine Maloney Leukemia virus, MMLV, and retroviruses that express the desirable properties of MMLV as a vector. Retroviral vectors are able to carry a larger genetic payload, i.e., a transgene or marker gene, than other viral vectors, and for this reason are a commonly used vector. However, they are not as useful in
30 non-proliferating cells. Adenovirus vectors are relatively stable and easy to work with, have high titers, and can be delivered in aerosol formulation, and can transfect non-dividing cells. Pox viral vectors are large and have several sites for inserting genes, they are thermostable and can be stored at room temperature. A preferred embodiment

is a viral vector which has been engineered so as to suppress the immune response of the host organism, elicited by the viral antigens.

Viral vectors can have higher transaction (ability to introduce genes) abilities than chemical or physical methods to introduce genes into cells. Typically, viral
5 vectors contain, nonstructural early genes, structural late genes, an RNA polymerase III transcript, inverted terminal repeats necessary for replication and encapsidation, and promoters to control the transcription and replication of the viral genome. When engineered as vectors, viruses typically have one or more of the early genes removed and a gene or gene/promotor cassette is inserted into the viral genome in place of the
10 removed viral DNA. Constructs of this type can carry up to about 8 kb of foreign genetic material. The necessary functions of the removed early genes are typically supplied by cell lines that have been engineered to express the gene products of the early genes in trans.

A retrovirus is an animal virus belonging to the virus family of Retroviridae,
15 including any types, subfamilies, genus, or tropisms. Retroviral vectors, in general, are described by Verma, I.M., Retroviral vectors for gene transfer. In Microbiology-1985, American Society for Microbiology, pp. 229-232, Washington, (1985), which is incorporated by reference herein. Examples of methods for using retroviral vectors for gene therapy are described in U.S. Patent Nos. 4,868,116 and 4,980,286; PCT
20 applications WO 90/02806 and WO 89/07136; and Mulligan, (Science 260:926-932 (1993)); the teachings of which are incorporated herein by reference. A retrovirus is essentially a package which has packed into it nucleic acid cargo. The nucleic acid cargo carries with it a packaging signal, which ensures that the replicated daughter molecules will be efficiently packaged within the package coat. In addition to the
25 package signal, there are a number of molecules that are needed in cis, for the replication, and packaging of the replicated virus. Typically a retroviral genome, contains the gag, pol, and env genes which are involved in the making of the protein coat. It is the gag, pol, and env genes which are typically replaced by the foreign DNA that it is to be transferred to the target cell. Retrovirus vectors typically contain a
30 packaging signal for incorporation into the package coat, a sequence which signals the start of the gag transcription unit, elements necessary for reverse transcription, including a primer binding site to bind the tRNA primer of reverse transcription, terminal repeat sequences that guide the switch of RNA strands during DNA synthesis,

a purine rich sequence 5' to the 3' LTR that serve as the priming site for the synthesis of the second strand of DNA synthesis, and specific sequences near the ends of the LTRs that enable the insertion of the DNA state of the retrovirus to insert into the host genome. The removal of the gag, pol, and env genes allows for about 8 kb of foreign
5 sequence to be inserted into the viral genome, become reverse transcribed, and upon replication be packaged into a new retroviral particle. This amount of nucleic acid is sufficient for the delivery of a one to many genes depending on the size of each transcript. It is preferable to include either positive or negative selectable markers along with other genes in the insert.

10 Since the replication machinery and packaging proteins in most retroviral vectors have been removed (gag, pol, and env), the vectors are typically generated by placing them into a packaging cell line. A packaging cell line is a cell line that has been transfected or transformed with a retrovirus that contains the replication and packaging machinery, but lacks any packaging signal. When the vector carrying the DNA of
15 choice is transfected into these cell lines, the vector containing the gene of interest is replicated and packaged into new retroviral particles, by the machinery provided in cis by the helper cell. The genomes for the machinery are not packaged because they lack the necessary signals.

The construction of replication-defective adenoviruses has been described
20 (Berkner et al., J. Virology 61:1213-1220 (1987); Massie et al., Mol. Cell. Biol. 6:2872-2883 (1986); Haj-Ahmad et al., J. Virology 57:267-274 (1986); Davidson et al., J. Virology 61:1226-1239 (1987); Zhang, Generation and identification of recombinant adenovirus by liposome-mediated transfection and PCR analysis, BioTechniques 15:868-872 (1993)). The benefit of the use of these viruses as vectors is that they are
25 limited in the extent to which they can spread to other cell types, since they can replicate within an initial infected cell, but are unable to form new infectious viral particles. Recombinant adenoviruses have been shown to achieve high efficiency gene transfer after direct, in vivo delivery to airway epithelium, hepatocytes, vascular endothelium, CNS parenchyma and a number of other tissue sites (Morsy, J. Clin.
30 Invest. 92:1580-1586 (1993); Kirshenbaum, J. Clin. Invest. 92:381-387 (1993); Roessler, J. Clin. Invest. 92:1085-1092 (1993); Moullier, Nature Genetics 4:154-159 (1993); La Salle, Science 259:988-990 (1993); Gomez-Foix, J. Biol. Chem. 267:25129-25134 (1992); Rich, Human Gene Therapy 4:461-476 (1993); Zabner,

Nature Genetics 6:75-83 (1994); Guzman, Circulation Research 73:1201-1207 (1993); Bout, Human Gene Therapy 5:3-10 (1994); Zabner, Cell 75:207-216 (1993); Caillaud, Eur. J. Neuroscience 5:1287-1291 (1993); and Ragot, J. Gen. Virology 74:501-507 (1993)). Recombinant adenoviruses achieve gene transduction by binding to specific cell surface receptors, after which the virus is internalized by receptor-mediated endocytosis, in the same manner as wild type or replication-defective adenovirus (Chardonnet and Dales, Virology 40:462-477 (1970); Brown and Burlingham, J. Virology 12:386-396 (1973); Svensson and Persson, J. Virology 55:442-449 (1985); Seth, et al., J. Virol. 51:650-655 (1984); Seth, et al., Mol. Cell. Biol. 4:1528-1533 (1984); Varga et al., J. Virology 65:6061-6070 (1991); Wickham et al., Cell 73:309-319 (1993)).

A viral vector can be one based on an adenovirus which has had the E1 gene removed and these virions are generated in a cell line such as the human 293 cell line. In another preferred embodiment both the E1 and E3 genes are removed from the adenovirus genome.

Another type of viral vector is based on an adeno-associated virus (AAV). This defective parvovirus is a preferred vector because it can infect many cell types and is nonpathogenic to humans. AAV type vectors can transport about 4 to 5 kb and wild type AAV is known to stably insert into chromosome 19. Vectors which contain this site specific integration property are preferred. An especially preferred embodiment of this type of vector is the P4.1 C vector produced by Avigen, San Francisco, CA, which can contain the herpes simplex virus thymidine kinase gene, HSV-tk, and/or a marker gene, such as the gene encoding the green fluorescent protein, GFP.

In another type of AAV virus, the AAV contains a pair of inverted terminal repeats (ITRs) which flank at least one cassette containing a promoter which directs cell-specific expression operably linked to a heterologous gene. Heterologous in this context refers to any nucleotide sequence or gene which is not native to the AAV or B19 parvovirus.

Typically the AAV and B19 coding regions have been deleted, resulting in a safe, noncytotoxic vector. The AAV ITRs, or modifications thereof, confer infectivity and site-specific integration, but not cytotoxicity, and the promoter directs cell-specific expression. United States Patent No. 6,261,834 is herein incorporated by reference for material related to the AAV vector.

Molecular genetic experiments with large human herpesviruses have provided a means whereby large heterologous DNA fragments can be cloned, propagated and established in cells permissive for infection with herpesviruses (Sun et al., Nature genetics 8: 33-41, 1994; Cotter and Robertson, Curr Opin Mol Ther 5: 633-644, 1999).

5 These large DNA viruses (herpes simplex virus (HSV) and Epstein-Barr virus (EBV), have the potential to deliver fragments of human heterologous DNA > 150 kb to specific cells. EBV recombinants can maintain large pieces of DNA in the infected B-cells as episomal DNA. Individual clones carried human genomic inserts up to 330 kb appeared genetically stable. The maintenance of these episomes requires a specific EBV
10 nuclear protein, EBNA1, constitutively expressed during infection with EBV. Additionally, these vectors can be used for transfection, where large amounts of protein can be generated transiently in vitro. Herpesvirus amplicon systems are also being used to package pieces of DNA > 220 kb and to infect cells that can stably maintain DNA as episomes. Other useful systems include, for example, replicating and host-restricted
15 non-replicating vaccinia virus vectors.

The invention also provides an isolated cell comprising a vector of the invention. The isolated cell can be either a eukaryotic or prokaryotic cell, such as strains of *E. coli*, *Pseudomonas*, *Bacillus*, *Streptomyces*; fungi such as yeasts (*Saccharomyces*, and methylotrophic yeast such as *Pichia*, *Candida*, *Hansenula*, and
20 *Torulopsis*); and animal cells, such as CHO, R1.1, B-W and LM cells, African Green Monkey kidney cells (for example, COS 1, COS 7, BSC1, BSC40, and BMT10), insect cells (for example, Sf9), and human cells and plant cells in tissue culture.

Also provided is a method of making a FcRH, or a fragment or variant thereof comprising culturing a cell comprising a vector of the invention under conditions
25 permitting expression of the FcRH. The method comprises culturing a cell comprising an exogenous nucleic acid that encodes the FcRH, fragment, or variant, wherein the exogenous nucleic acid is operably linked to an expression control sequence, and wherein the culture conditions permit expression of the FcRH, fragment, or variant under the control of the expression control sequence; harvesting the medium from the
30 cultured cells, and isolating the FcRH, fragment, or variant from the cell or culture medium. Optionally the exogenous nucleic acid is the nucleotide sequence of SEQ ID NO:7, SEQ ID NO:13, SEQ ID NO:8, SEQ ID NO:34, SEQ ID NO:9, SEQ ID NO:14, SEQ ID NO:10, SEQ ID NO:36, SEQ ID NO:11, SEQ ID NO:15, SEQ ID NO:16, SEQ

ID NO:12, SEQ ID NO:38, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, and SEQ ID NO:20; SEQ ID NO:40, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, or SEQ ID NO:102 or a combination thereof. Optionally, the exogenous nucleic acid further comprises a nucleotide sequence that encodes a signal sequence. In the recombinant methods, the cell can be any known host cell, including for example, a prokaryotic or eukaryotic cell. The nucleic acids that are delivered to cells, generally in a plasmid or other vector, typically contain expression controlling systems. For example, the inserted genes in viral and retroviral systems usually contain promoters, and/or enhancers to help control the expression of the desired gene product.

Those skilled in the art of molecular biology will understand that a wide variety of expression systems may be used to produce recombinant FcRH polypeptides (as well as fragments, fusion proteins, and amino acid sequence variants with therapeutic activity) for use in the methods of the invention. Thus, FcRH may be produced using prokaryotic host cells (e.g., *Escherichia coli*) or eukaryotic host cells (e.g., *Saccharomyces cerevisiae*, insect cells such as Sf9 cells, or mammalian cells such as CHO cells, COS-1, NIH 3T3, or HeLa cells). These cells are commercially available from, for example, the American Type Culture Collection, Rockville, MD (see also F. Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, NY, 1998). The method of transformation and the choice of expression vector will depend on the host system selected. Transformation and transfection methods are described, e.g., in Ausubel et al., *supra*, and expression vectors may be chosen from the numerous examples known in the art.

A nucleic acid sequence encoding an FcRH is introduced into a plasmid or other vector, which is then used to transform living cells. Constructs in which a cDNA containing the entire FcRH coding sequence, a fragment of the FcRH coding sequence, amino acid variations of the FcRH coding sequence, or fusion proteins of the aforementioned, inserted in the correct orientation into an expression plasmid, may be used for protein expression. In some cases, for example, it may be desirable to express the FcRH coding sequence under the control of an inducible or tissue-specific promoter.

Eukaryotic expression systems permit appropriate post-translational modifications to expressed proteins. Thus, eukaryotic, and more preferably mammalian expression systems, allow glycosylation patterns comparable to naturally expressed FcRH. Transient transfection of a eukaryotic expression plasmid allows the transient production of FcRH by a transfected host cell. FcRH may also be produced by a stably-transfected mammalian cell line. A number of vectors suitable for stable transfection of mammalian cells are available to the public (e.g., see Pouwels et al., *Cloning Vectors: A Laboratory Manual*, 1985, Supp. 1987), as are methods for constructing such cell lines (see e.g., F. Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, NY, 1998). Another preferred eukaryotic expression system is the baculovirus system using, for example, the vector pBacPAK9, which is available from Clontech (Palo Alto, CA). If desired, this system may be used in conjunction with other protein expression techniques, for example, the myc tag approach described by Evan et al. (*Mol. Cell Biol.* 5:3610-3616, 1985) or analogous tagging approaches, e.g., using a hemagglutinin (HA) tag.

Once the recombinant protein is expressed, it can be isolated from the expressing cells by cell lysis followed by protein purification techniques such as affinity chromatography. In this example, an antibody that specifically binds to FcRH, which may be produced by methods that are well-known in the art, can be attached to a column and used to isolate FcRH. Once isolated, the recombinant protein can, if desired, be purified further, e.g., by high performance liquid chromatography (HPLC; e.g., see Fisher, *Laboratory Techniques In Biochemistry And Molecular Biology*, Work and Burdon, Eds., Elsevier, 1980).

Antibodies

The invention also provides a purified antibody or immunologic fragment thereof, wherein the antibody or fragment thereof selectively binds to an FcRH. As used herein, the term "antibody" encompasses, but is not limited to, whole immunoglobulin (i.e., an intact antibody) of any class. Native antibodies are usually heterotetrameric glycoproteins, composed of two identical light (L) chains and two identical heavy (H) chains. Typically, each light chain is linked to a heavy chain by one covalent disulfide bond, while the number of disulfide linkages varies between the heavy chains of different immunoglobulin isotypes. Each heavy and light chain also

has regularly spaced intrachain disulfide bridges. Each heavy chain has at one end a variable domain ($V(H)$) followed by a number of constant domains. Each light chain has a variable domain at one end ($V(L)$) and a constant domain at its other end; the constant domain of the light chain is aligned with the first constant domain of the heavy chain, and the light chain variable domain is aligned with the variable domain of the heavy chain. Particular amino acid residues are believed to form an interface between the light and heavy chain variable domains. The light chains of antibodies from any vertebrate species can be assigned to one of two clearly distinct types, called kappa (κ) and lambda (λ), based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG-1, IgG-2, IgG-3, and IgG-4; IgA-1 and IgA-2. The heavy chain constant domains that correspond to the different classes of immunoglobulins are called alpha, delta, epsilon, gamma, and mu, respectively.

The term "variable" is used herein to describe certain portions of the variable domains that differ in sequence among antibodies and are used in the binding and specificity of each particular antibody for its particular antigen. However, the variability is not usually evenly distributed through the variable domains of antibodies.

It is typically concentrated in three segments called complementarity determining regions (CDRs) or hypervariable regions both in the light chain and the heavy chain variable domains. The more highly conserved portions of the variable domains are called the framework (FR). The variable domains of native heavy and light chains each comprise four FR regions, largely adopting a β -sheet configuration, connected by three CDRs, which form loops connecting, and in some cases forming part of, the β -sheet structure. The CDRs in each chain are held together in close proximity by the FR regions and, with the CDRs from the other chain, contribute to the formation of the antigen binding site of antibodies (see Kabat E. A. et al., "Sequences of Proteins of Immunological Interest" National Institutes of Health, Bethesda, Md. (1987)). The constant domains are not involved directly in binding an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody-dependent cellular toxicity.

The term "antibody or fragments thereof" can also encompass chimeric antibodies and hybrid antibodies, with dual or multiple antigen or epitope specificities, and fragments, such as F(ab')₂, Fab', Fab and the like, including hybrid fragments.

Thus, fragments of the antibodies that retain the ability to bind their specific antigens are provided. For example, fragments of antibodies which maintain FcRH binding activity are included within the meaning of the term "antibody or fragment thereof." Such antibodies and fragments can be made by techniques known in the art and can be screened for specificity and activity according to the methods set forth in the Examples and in general methods for producing antibodies and screening antibodies for specificity and activity (See Harlow and Lane. Antibodies, A Laboratory Manual. Cold Spring Harbor Publications, New York, (1988)).

Also included within the meaning of "antibody or fragments thereof" are conjugates of antibody fragments and antigen binding proteins (single chain antibodies) as described, for example, in U.S. Pat. No. 4,704,692, the contents of which are hereby incorporated by reference.

In one embodiment, the antibody is a monoclonal antibody. The term "monoclonal antibody" as used herein refers to an antibody obtained from a substantially homogeneous population of antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. The monoclonal antibodies herein specifically include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired activity (See, U.S. Pat. No. 4,816,567 and Morrison et al., Proc. Natl. Acad. Sci. USA, 81:6851-6855 (1984)).

Monoclonal antibodies of the invention may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975) or Harlow and Lane, Antibodies, A Laboratory Manual. Cold Spring Harbor Publications, New York, (1988). In a hybridoma method, a mouse or other appropriate host animal,

is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*. Preferably, the immunizing agent comprises an FcRH. Traditionally, the generation of monoclonal antibodies has depended on the availability of purified protein or peptides for use as the immunogen. More recently DNA based immunizations have shown promise as a way to elicit strong immune responses and generate monoclonal antibodies. In this approach, DNA-based immunization can be used, wherein DNA encoding a portion of FcRH, preferably the N- or C- terminal region, is injected into the host animal according to methods known in the art.

Generally, either peripheral blood lymphocytes ("PBLs") are used in methods of producing monoclonal antibodies if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, "Monoclonal Antibodies: Principles and Practice" Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, including myeloma cells of rodent, bovine, equine, and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, Calif. and the American Type Culture Collection, Rockville, Md. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J.

Immunol., 133:3001 (1984); Brodeur et al., "Monoclonal Antibody Production Techniques and Applications" Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against an FcRH.

5 Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art, and are described further in Harlow and Lane "Antibodies, A Laboratory Manual" Cold Spring Harbor Publications, New York,
10 (1988).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution or FACS sorting procedures and grown by standard methods. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.
15

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

20 The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Pat. No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The
25 hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, plasmacytoma cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells.
30 The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Pat. No. 4,816,567) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin

polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody comprising one antigen-combining site having specificity
5 for FcRH and another antigen-combining site having specificity for a different antigen.

In vitro methods are also suitable for preparing monovalent antibodies.

Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art. For instance, digestion can be performed using papain. Examples of papain digestion are described in WO
10 94/29348 published Dec. 22, 1994, U.S. Pat. No. 4,342,566, and Harlow and Lane, Antibodies, A Laboratory Manual, Cold Spring Harbor Publications, New York, (1988). Papain digestion of antibodies typically produces two identical antigen binding fragments, called Fab fragments, each with a single antigen binding site, and a residual Fc fragment. Pepsin treatment yields a fragment, called the F(ab')₂ fragment, that has
15 two antigen combining sites and is still capable of cross-linking antigen.

The Fab fragments produced in the antibody digestion also contain the constant domains of the light chain and the first constant domain of the heavy chain. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain domain including one or more cysteines from the antibody
20 hinge region. The F(ab')₂ fragment is a bivalent fragment comprising two Fab' fragments linked by a disulfide bridge at the hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. Antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments
25 are also known.

An isolated immunogenically specific epitope or fragment of the antibody is also provided. A specific immunogenic epitope of the antibody can be isolated from the whole antibody by chemical or mechanical disruption of the molecule. The purified fragments thus obtained can be tested to determine their immunogenicity and specificity
30 by the methods taught herein. Immunoreactive epitopes of the antibody can also be synthesized directly. An immunoreactive fragment is defined as an amino acid sequence of at least about two to five consecutive amino acids derived from the antibody amino acid sequence.

One method of producing proteins comprising the antibodies of the present invention is to link two or more peptides or polypeptides together by protein chemistry techniques. For example, peptides or polypeptides can be chemically synthesized using currently available laboratory equipment using either Fmoc (9-fluorenylmethyl-oxycarbonyl) or Boc (*tert*-butoxycarbonyl) chemistry. (Applied Biosystems, Inc., Foster City, CA). One skilled in the art can readily appreciate that a peptide or polypeptide corresponding to the antibody of the present invention, for example, can be synthesized by standard chemical reactions. For example, a peptide or polypeptide can be synthesized and not cleaved from its synthesis resin whereas the other fragment of an antibody can be synthesized and subsequently cleaved from the resin, thereby exposing a terminal group that is functionally blocked on the other fragment. By peptide condensation reactions, these two fragments can be covalently joined via a peptide bond at their carboxyl and amino termini, respectively, to form an antibody, or fragment thereof. (Grant GA (1992) *Synthetic Peptides: A User Guide*. W.H. Freeman and Co., N.Y. (1992); Bodansky M and Trost B., Ed. (1993) *Principles of Peptide Synthesis*. Springer-Verlag Inc., NY). Alternatively, the peptide or polypeptide can be independently synthesized *in vivo* as described above. Once isolated, these independent peptides or polypeptides may be linked to form an antibody or fragment thereof via similar peptide condensation reactions.

For example, enzymatic ligation of cloned or synthetic peptide segments can allow relatively short peptide fragments to be joined to produce larger peptide fragments, polypeptides or whole protein domains (Abrahmsen L et al., *Biochemistry*, 30:4151 (1991)). Alternatively, native chemical ligation of synthetic peptides can be utilized to synthetically construct large peptides or polypeptides from shorter peptide fragments. This method consists of a two step chemical reaction (Dawson et al. *Synthesis of Proteins by Native Chemical Ligation*. *Science*, 266:776-779 (1994)). The first step is the chemoselective reaction of an unprotected synthetic peptide- α -thioester with another unprotected peptide segment containing an amino-terminal Cys residue to give a thioester-linked intermediate as the initial covalent product. Without a change in the reaction conditions, this intermediate undergoes spontaneous, rapid intramolecular reaction to form a native peptide bond at the ligation site. Application of this native chemical ligation method to the total synthesis of a protein molecule is illustrated by the preparation of human interleukin 8 (IL-8) (Baggiolini M et al. (1992) *FEBS Lett.*

307:97-101; Clark-Lewis I et al., J.Biol.Chem., 269:16075 (1994); Clark-Lewis I et al., Biochemistry, 30:3128 (1991); Rajarathnam K et al., Biochemistry 33:6623-30 (1994)).

Alternatively, unprotected peptide segments can be chemically linked where the bond formed between the peptide segments as a result of the chemical ligation is an unnatural (non-peptide) bond (Schnolzer, M et al. Science, 256:221 (1992)). This technique has been used to synthesize analogs of protein domains as well as large amounts of relatively pure proteins with full biological activity (deLisle Milton RC et al., Techniques in Protein Chemistry IV. Academic Press, New York, pp. 257-267 (1992)).

The invention also provides fragments of antibodies that have bioactivity. The polypeptide fragments of the present invention can be recombinant proteins obtained by cloning nucleic acids encoding the polypeptide in an expression system capable of producing the polypeptide fragments thereof, such as an adenovirus or baculovirus expression system. For example, one can determine the active domain of an antibody from a specific hybridoma that can cause a biological effect associated with the interaction of the antibody with FcRH. For example, amino acids found to not contribute to either the activity or the binding specificity or affinity of the antibody can be deleted without a loss in the respective activity.

For example, amino or carboxy-terminal amino acids can be sequentially removed from either the native or the modified non-immunoglobulin molecule or the immunoglobulin molecule and the respective activity assayed in one of many available assays. In another example, a fragment of an antibody can comprise a modified antibody wherein at least one amino acid has been substituted for the naturally occurring amino acid at a specific position, and a portion of either amino terminal or carboxy terminal amino acids, or even an internal region of the antibody, has been replaced with a polypeptide fragment or other moiety, such as biotin, which can facilitate in the purification of the modified antibody. For example, a modified antibody can be fused to a maltose binding protein, through either peptide chemistry of cloning the respective nucleic acids encoding the two polypeptide fragments into an expression vector such that the expression of the coding region results in a hybrid polypeptide. The hybrid polypeptide can be affinity purified by passing it over an amylose affinity column, and the modified antibody receptor can then be separated from the maltose binding region by cleaving the hybrid polypeptide with the specific protease

factor Xa. (See, for example, New England Biolabs Product Catalog, 1996, pg. 164.). Similar purification procedures are available for isolating hybrid proteins from eukaryotic cells as well.

The fragments, whether attached to other sequences, can also include insertions, deletions, substitutions, or other selected modifications of particular regions or specific amino acids residues, provided the activity of the fragment is not significantly altered or impaired compared to the nonmodified antibody or antibody fragment. These modifications can provide for some additional property, such as to remove or add amino acids capable of disulfide bonding, to increase its bio-longevity, to alter its secretory characteristics, etc. In any case, the fragment must possess a bioactive property, such as binding activity, regulation of binding at the binding domain, etc. Functional or active regions of the antibody may be identified by mutagenesis of a specific region of the protein, followed by expression and testing of the expressed polypeptide. Such methods are readily apparent to a skilled practitioner in the art and can include site-specific mutagenesis of the nucleic acid encoding the antigen. (Zoller MJ et al. Nucl. Acids Res. 10:6487-500 (1982).

As used herein, the phrase "specific binding" or "selective binding" refers to a binding reaction which is determinative of the presence of the FcRH in a heterogeneous population of proteins and other biologics. Thus, under designated conditions, the antibodies or fragments thereof of the present invention bind to a particular FcRH (e.g., human FcRH 1 or any variant thereof), fragment, or variant thereof and do not bind in a significant amount to other proteins (e.g., human FcRH 2, 3, 4, 5, or 6), present in the subject. The absence of binding in the present invention is considered to be binding that is less than 1.5 times background (i.e., the level of non-specific binding or slightly above non-specific binding levels),

Selective binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein, variant, or fragment. In one embodiment the purified antibody selectively binds to the FcRH comprising a cytoplasmic region with more than 107 or less than 104 amino acids, a transmembrane region, and an extracellular region. More specifically, the antibody in alternative embodiments selectively binds FcRH1 but not FcRH2-6; selectively binds FcRH2 but not 1 or 3-6; selectively binds FcRH3 but not FcRH1-2 or 4-6; selectively binds FcRH6 but not 1-5. Thus, as one embodiment, the antibody selectively binds a polypeptide

comprising the amino acid sequence of SEQ ID NO:1, 21, or 2, or a subset thereof, but not to polypeptides comprising the amino acid of SEQ ID NO:3, 22, 4, 5, 23, 24, 6, 25, 26, 27, 28, or a subset thereof. In another embodiment the purified antibody binds to the FcRH comprising the amino acid sequence of SEQ ID NO:3, 22, or 4, but not to the FcRH comprising the amino acid of SEQ ID NO:1, 21, 2, 5, 23, 24, 6, 25, 26, 27, or 28. In yet another embodiment, the purified antibody that binds to the FcRH comprising the amino acid sequence of SEQ ID NO:5, 23, 24, or 6, but not to the FcRH comprising the amino acid of SEQ ID NO:1, 21, 2, 3, 22, 4, 26, 27, 28. Similarly, the antibodies of the present invention may bind only moFcRH1, but not moFcRH 2 or moFcRH3; may bind only FcRH2 and not FcRH1 or FcRH3, and may bind only FcRH3 and not FcRH1 or FcRH2.

In certain embodiments, the antibody binds the extracellular region of one or more FcRHs and in other embodiments the antibody binds the cytoplasmic region of one or more FcRHs. In other embodiments the antibody may selectively bind one isoform of a FcRH. For example, the antibody may bind a polypeptide having the amino acid sequence of SEQ ID NO:23 but not the SEQ ID NO:24 or vice versa. Furthermore, the antibody can bind to moFcRH1 having the amino acid sequence of SEQ ID NO:70, but not to a moFcRH1 having amino acid sequence of SEQ ID NO:68. The antibody may selectively bind a moFcRH2 with a transmembrane region (e.g., having amino acid sequence of SEQ ID NO:73), but not bind to a moFcRH2 lacking a transmembrane region (e.g., having the amino acid sequence of 77). Optionally the antibody of the invention can selectively bind moFcRH but not human, or vice versa.

A variety of immunoassay formats may be used to select antibodies that selectively bind with a particular protein, variant, or fragment. For example, solid-phase ELISA immunoassays are routinely used to select antibodies selectively immunoreactive with a protein, variant, or fragment thereof. See Harlow and Lane. Antibodies, A Laboratory Manual. Cold Spring Harbor Publications, New York, (1988), for a description of immunoassay formats and conditions that could be used to determine selective binding. The binding affinity of a monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson et al., Anal. Biochem., 107:220 (1980).

The invention also provides an antibody reagent kit comprising the antibody or fragment thereof of the invention and reagents for detecting binding of the antibody or

fragment thereof to a ligand. The kit can further comprise containers containing the antibody or fragment thereof of the invention and containers containing the reagents. Preferably the ligand is a FcRH, variant, or fragment thereof. Particularly, the kit can detect the presence of one or more FcRHs specifically reactive with the antibody or an immunoreactive fragment thereof. The kit can include an antibody bound to a substrate, a secondary antibody reactive with the antigen and a reagent for detecting a reaction of the secondary antibody with the antigen. Such a kit can be an ELISA kit and can comprise the substrate, primary and secondary antibodies when appropriate, and any other necessary reagents such as detectable moieties, enzyme substrates and color reagents as described above. The diagnostic kit can, alternatively, be an immunoblot kit generally comprising the components and reagents described herein. Alternatively, the kit could be a radioimmunoassay kit, a Western blot assay kit, an immunohistological assay kit, an immunocytochemical assay kit, a dot blot assay kit, a fluorescence polarization assay kit, a scintillation proximity assay kit, a homogeneous time resolved fluorescence assay kit, or a BIAcore analysis kit.

As used throughout, methods of detecting an FcRH or antigen/antibody complexes, including complexes comprising an FcRH and optionally the antibody of the present invention, can comprise an ELISA (competition or sandwich), a radioimmunoassay, a Western blot assay, an immunohistological assay, an immunocytochemical assay, a dot blot assay, a fluorescence polarization assay (Jolley (1981); Jiskoot et al (1991); Seethala et al. (1998); Bicamumpaka et al. (1998)), a scintillation proximity assay (Amersham Life Science (1995) Proximity News. Issue 17; Amersham Life Science (1995) Proximity News. Issue 18; Park et al. (1999)), a homogeneous time-resolved fluorescence assay (Park et al. (1999); Stenroos et al. (1988); Morrison, 1988)), or a BIAcore analysis (Fägerstam et al. (1992) Chromatography 597:397-410. Preferably, the antigen/antibody complex is detectably tagged either directly or indirectly. Any desired tag can be utilized, such as a fluorescent tag, a radiolabel, a magnetic tag, or an enzymatic reaction product.

Optionally, the antibody or fragment is a humanized antibody or a fully human antibody. For example, the antibodies can also be generated in other species and "humanized" for administration to humans. Alternatively, fully human antibodies can also be made by immunizing a mice or other species capable of making a fully human antibody (e.g., mice genetically modified to produce human antibodies), screening

clones that bind FcRH. See, e.g., Lonberg and Huszar (1995) Human antibodies from transgenic mice, *Int. Rev. Immunol.* 13:65-93, which is incorporated herein by reference in its entirety for methods of producing fully human antibodies. As used herein, the term "humanized" and "fully human" in relation to antibodies, relate to any
5 antibody which is expected to elicit a therapeutically tolerable weak immunogenic response in a human subject.

Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂, or other antigen-binding subsequences of antibodies) which contain minimal
10 sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the
15 human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all or at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to
20 those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)).
25

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source that is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable
30 domain. Humanization can be essentially performed following the method of Winter and co-workers (Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeyen et al., *Science*, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody.

Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Pat. No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

The choice of human variable domains, both light and heavy, to be used in making the humanized antibodies is very important in order to reduce antigenicity. According to the "best-fit" method, the sequence of the variable domain of a rodent antibody is screened against the entire library of known human variable domain sequences. The human sequence which is closest to that of the rodent is then accepted as the human framework (FR) for the humanized antibody (Sims et al., J. Immunol., 151:2296 (1993) and Chothia et al., J. Mol. Biol., 196:901 (1987)). Another method uses a particular framework derived from the consensus sequence of all human antibodies of a particular subgroup of light or heavy chains. The same framework may be used for several different humanized antibodies (*Carter et al.*, Proc. Natl. Acad. Sci. USA, 89:4285 (1992); Presta et al., J. Immunol., 151:2623 (1993)).

It is further important that antibodies be humanized with retention of high affinity for the antigen and other favorable biological properties. To achieve this goal, according to a preferred method, humanized antibodies are prepared by a process of analysis of the parental sequences and various conceptual humanized products using three dimensional models of the parental and humanized sequences. Three dimensional immunoglobulin models are commonly available and are familiar to those skilled in the art. Computer programs are available which illustrate and display probable three-dimensional conformational structures of selected candidate immunoglobulin sequences. Inspection of these displays permits analysis of the likely role of the residues in the functioning of the candidate immunoglobulin sequence, i.e., the analysis of residues that influence the ability of the candidate immunoglobulin to bind its antigen. In this way, FR residues can be selected and combined from the consensus and import sequence so that the desired antibody characteristic, such as increased affinity for the target antigen(s), is achieved. In general, the CDR residues are directly and most substantially involved in influencing antigen binding (see, WO 94/04679 published 3 Mar. 1994).

Transgenic animals (e.g., mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production can be employed. For example, it has been described that the homozygous deletion of the antibody heavy chain joining region (*J(H)*) gene in
5 chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array in such germ-line mutant mice will result in the production of human antibodies upon antigen challenge (see, e.g., Jakobovits et al., Proc. Natl. Acad. Sci. USA, 90:2551-255 (1993); Jakobovits et al., Nature, 362:255-258 (1993); Bruggemann et al., Year in
10 Immuno., 7:33 (1993)). Human antibodies can also be produced in phage display libraries (Hoogenboom et al., J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). The techniques of Cote et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985); Boerner et al., J. Immunol., 147(1):86-
15 95 (1991)).

In one embodiment, the antibody or fragment thereof is a single chain antibody. In another embodiment, the antibody or fragment is labeled. Optionally the antibody or fragment is conjugated or fused with a toxin or fragment thereof. Examples of the toxin or toxin moiety include diphtheria, ricin, and modifications thereof.

20

Diagnosis and Treatment

The invention provides uses of the reagents described herein in *in vitro* and *in vivo* methods of diagnosing and treating a malignancy of hematopoietic cell lineage or an autoimmune disease in a subject. The reagents of the present invention are also
25 useful in screening for disease manifestations. Such screening may be useful even before the onset of other clinical symptoms and could be used to screening subjects at risk for disease, so that prophylactic treatment can be started before the manifestation of other signs or symptoms.

By "malignancy" is meant a tumor or neoplasm whose cells possess one or more
30 nuclear or cytoplasmic abnormalities, including, for example, high nuclear to cytoplasmic ratio, prominent nucleolar/nucleoli variations, variations in nuclear size, abnormal mitotic figures, or multinucleation. "Malignancies of hematopoietic cell lineage" include, but are not limited to, myelomas, leukemias, lymphomas (Hodgkin's

and non-Hodgkin's forms), T-cell malignancies, B-cell malignancies, and lymphosarcomas or other malignancies described in the REAL classification system or the World Health Organization Classification of Hematologic Malignancies. It should be noted that the absence or presence of specific FcRHs can be diagnostic for a particular malignancy of hematopoietic cell lineage or can be diagnostic for a particular form of a malignancy (e.g., a specific form of leukemia).

By "inflammatory and autoimmune diseases" illustratively including systemic lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-host disease, Sjögren's syndrome, pernicious anemia, Addison disease, scleroderma, Goodpasture's syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin-dependent diabetes mellitus, allergy; asthma, atopic disease; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anemia; rejection after organ transplantation and numerous malignancies of lung, prostate, liver, ovary, colon, cervix, lymphatic and breast tissues.

Specifically, the diagnostic methods comprise the steps of contacting a biological sample of the subject with an antibody or nucleic acid of the invention under conditions that allow the antibody to bind to cells of hematopoietic cell lineage or allow the nucleic acid to hybridize, preferably under stringent conditions, with nucleic acids of the biological sample; and detecting the amount or pattern of binding. Changes in the amount or pattern of binding as compared to binding in a control sample indicate a malignancy or an inflammatory or autoimmune disease.

In various embodiments, the antibody used in the diagnostic method can selectively bind with an FcRH having the amino acid sequence of SEQ ID NO:1, 21, 2, 3, 22, 4, 5, 24, or 6.

The detecting step of the diagnostic method can be selected from methods routine in the art. For example, the detection step can be performed *in vivo* using a noninvasive medical technique such as radiography, fluoroscopy, sonography, imaging techniques such as magnetic resonance imaging, and the like. *In vitro* detection methods can be used to detect bound antibody or fragment thereof in an ELISA, RIA, immunohistochemically, FACS, IHC, FISH, or similar assays.

As used throughout, "biological sample" refers to a sample from any organism. The sample can be, but is not limited to, peripheral blood, plasma, urine, saliva, gastric

secretion, feces, bone marrow specimens, primary tumors, embedded tissue sections, frozen tissue sections, cell preparations, cytological preparations, exfoliate samples (e.g., sputum), fine needle aspirations, amnion cells, fresh tissue, dry tissue, and cultured cells or tissue. It is further contemplated that the biological sample of this invention can also be whole cells or cell organelles (e.g., nuclei). The sample can be unfixed or fixed according to standard protocols widely available in the art and can also be embedded in a suitable medium for preparation of the sample. For example, the sample can be embedded in paraffin or other suitable medium (e.g., epoxy or acrylamide) to facilitate preparation of the biological specimen for the detection methods of this invention.

The invention also provides a method of treating a malignancy of hematopoietic cell lineage or an inflammatory or autoimmune disease in a subject, comprising contacting the subject's malignant cells or inflammatory cells with a therapeutically effective amount of a reagent (e.g., an antibody or nucleic acid) or a therapeutic composition of a reagent of the invention. The contacting step can occur by administration of the reagent or composition using any number of means available in the art. Typically, the reagent or composition is administered to the subject transdermally (e.g., by a transdermal patch or a topically applied cream, ointment, or the like), orally, subcutaneously, intrapulmonaryly, transmucosally, intraperitoneally, intrauterinely, sublingually, intrathecally, intramuscularly, intraarticularly, etc. using conventional methods. In addition, the reagent or composition can be administered via injectable depot routes such as by using 1-, 3-, or 6-month depot injectable or biodegradable materials and methods.

Regardless of the route of administration, the amount of the reagent administered or the schedule for administration will vary among individuals based on age, size, weight, condition to be treated, mode of administration, and the severity of the condition. One skilled in the art will realize that dosages are best optimized by the practicing physician and methods for determining dosage are described, for example in Remington's Pharmaceutical Science, latest edition. Guidance in selecting appropriate doses for antibodies is found in the literature on therapeutic uses of antibodies, e.g., Handbook of Monoclonal Antibodies, Ferrone et al., eds., Noyes Publications, Park Ridge, N.J., (1985) ch. 22 and pp. 303-357; Smith et al., Antibodies in Human Diagnosis and Therapy, Haber et al., eds., Raven Press, New York (1977) pp. 365-389. A typical dose of

the antibody used alone might range from about 1 µg/kg to up to 100 mg/kg of body weight or more per day, and preferably 1 µg/kg to up to 1 mg/kg, depending on the factors mentioned above. An intravenous injection of the antibody or fragment thereof, for example, could be 10ng-1g of antibody or fragment thereof, and preferably 10ng-1mg
5 depending on the factors mentioned above. For local injection, a typical quantity of antibody ranges from 1pg to 1mg . Preferably, the local injection would be at an antibody concentration of 1-100 µg/ml, and preferably 1-20 µg/ml.

The nucleic acids of the invention can delivered to cells in a variety of ways. For example, if the nucleic acid of this invention is delivered to the cells of a subject in
10 an adenovirus vector, the dosage for administration of adenovirus to humans can range from about 10^7 to 10^9 plaque forming units (pfu) per injection, but can be as high as 10^{12} pfu per injection. Ideally, a subject will receive a single injection. If additional injections are necessary, they can be repeated at six month intervals for an indefinite period and/or until the efficacy of the treatment has been established. As set forth
15 herein, the efficacy of treatment can be determined by evaluating the clinical parameters.

The exact amount of the nucleic acid or vector required will vary as described above. Thus, it is not possible to specify an exact amount for every nucleic acid or vector. An appropriate amount can be determined by one of ordinary skill in the art
20 using only routine experimentation given the teachings herein.

The invention further provides a therapeutic composition of the reagent of the invention. Such a composition typically contains from about 0.1 to 90% by weight (such as 1 to 20% or 1 to 10%) of a therapeutic agent of the invention in a pharmaceutically acceptable carrier. Solid formulations of the compositions for oral
25 administration may contain suitable carriers or excipients, such as corn starch, gelatin, lactose, acacia, sucrose, microcrystalline cellulose, kaolin, mannitol, dicalcium phosphate, calcium carbonate, sodium chloride, or alginic acid. Disintegrators that can be used include, without limitation, microcrystalline cellulose, corn starch, sodium starch, glycolate, and alginic acid. Tablet binders that may be used include acacia,
30 methylcellulose, sodium carboxymethylcellulose, polyvinylpyrrolindone (PovidoneTM), hydroxypropyl methylcellulose, sucrose, starch, and ethylcellulose. Lubricants that may be used include magnesium stearates, stearic acid, silicone fluid, talc, waxes, oils, and colloidal silica.

Liquid formulations for oral administration prepared in water or other aqueous vehicles may contain various suspending agents such as methylcellulose, alginates, tragacanth, pectin, kelgin, carrageenan, acacia, polyvinylpyrrolidone, and polyvinyl alcohol. The liquid formulations may also include solutions, emulsions, syrups and
5 elixirs containing, together with the active compound(s), wetting agents, sweeteners, and coloring and flavoring agents. Various liquid and powder formulations can be prepared by conventional methods for inhalation into the lungs of the mammal to be treated.

Injectable formulations of the compositions may contain various carriers such as
10 vegetable oils, dimethylacetamide, dimethylformamide, ethyl lactate, ethyl carbonate, isopropyl myristate, ethanol, polyols (glycerol, propylene glycol, liquid polyethylene glycol, and the like). For intravenous injections, water soluble version of the compounds may be administered by the drip method, whereby a pharmaceutical formulation containing the antifungal agent and a physiologically acceptable excipient
15 is infused. Physiologically acceptable excipients may include, for example, 5% dextrose, 0.9% saline, Ringer's solution or other suitable excipients. Intramuscular preparations, e.g., a sterile formulation of a suitable soluble salt form of the compounds, can be dissolved and administered in a pharmaceutical excipient such as water-for-injection, 0.9% saline, or 5% glucose solution. A suitable insoluble form of the
20 compound may be prepared and administered as a suspension in an aqueous base or a pharmaceutically acceptable oil base, such as an ester of a long chain fatty acid (e.g., ethyl; oleate).

A topical semi-solid ointment formulation typically contains a concentration of the active ingredient from about 1 to 20%, e.g., 5 to 10%, in a carrier such as a
25 pharmaceutical cream base. Various formulations for topical use include drops, tinctures, lotions, creams, solutions, and ointments containing the active ingredient and various supports and vehicles. The optimal percentage of the therapeutic agent in each pharmaceutical formulation varies according to the formulation itself and the therapeutic effect desired in the specific pathologies and correlated therapeutic
30 regimens.

The effectiveness of the method of treatment can be assessed by monitoring the patient for known signs or symptoms of the conditions being treated. For example, in the treatment of a malignancy of hematopoietic cell lineage, the reduction or

stabilization of the number of abnormally proliferative cells would indicate successful treatment. In the treatment of arthritis, for example, a reduction in the amount of joint inflammation would indicate successful treatment. Thus, by "therapeutically effective" is meant an amount that provides the desired treatment effect.

5 The invention further provides a method of modulating a humoral immune response in a subject, comprising administering to the subject an isolated FcRH, an antibody, or nucleic acid of the invention. By "modulation" is meant either up-regulating or down-regulating. Thus, in the case of an allergic response, one skilled in the art would choose to down-regulate the humoral immune response. In the case of
10 exposure of a subject to an infectious agent (e.g., a viral or bacterial agent), one skilled in the art would choose to upregulate the humoral antibody response.

Experimental

15 The following examples are put forth so as to provide those of ordinary skill in the art with a complete disclosure and description of how the compounds, compositions, articles, devices and/or methods claimed herein are made and evaluated, and are intended to be purely exemplary of the invention and are not intended to limit the scope of what the inventors regard as their invention. Efforts have been made to ensure accuracy with respect to numbers (e.g., amounts, temperature, etc.), but some
20 errors and deviations should be accounted for. Unless indicated otherwise, parts are parts by weight, temperature is in °C or is at ambient temperature, and pressure is at or near atmospheric.

EXAMPLE 1

25 Identification of FcRH1, FcRH2, and FcRH3

 In order to isolation of FcRH cDNA Clones, rapid amplification of cDNA ends (RACE)-PCR was performed by using a Marathon-Ready human lymph node cDNA library (CLONTECH). Gene-specific primers were as follows: FcRH3, forward 5'-TGAGTCTCAGGGTCACAGTTCCG-3' (SEQ ID NO:41) and reverse 5'-
30 GCTCTTGAACCTGGATATTTAGGGGT-3' (SEQ ID NO:42); FcRH2, forward 5'-CCAGTGTATGTCAATGTGGGCTCTG-3' (SEQ ID NO:43) and reverse 5'-CGTTGAAAGAGCTCTTGGACTTTTATC-3' (SEQ ID NO:44); and FcRH1, forward 5'-GCCTCAAAAGAAAAATAGGAAGACGTT-3' (SEQ ID NO:45) and reverse 5'-

AAGCTCACATCAGCGACAGGGAC-3' (SEQ ID NO:46). RACE products were subjected to a second round of nested PCR and visualized by agarose gel electrophoresis and ethidium bromide staining.

Primers used in end-to-end amplification to generate full-length cDNAs were as follows: FcRH3, forward 5'-TCTTGGAGATAAGTCGGGCTTT-3' (SEQ ID NO:47) and reverse 5'-ATCCTGCAGCCCAGCCTCGTAGGAG-3' (SEQ ID NO:48); FcRH2, forward 5'-GGTCCTCATGCTGCTGTGGTCATT-3' (SEQ ID NO:49) and reverse 5'-GCTGTTGATCTTCCCTTCTGATT-3' (SEQ ID NO:50); and FcRH1, forward 5'-ATGCTGCCGAGGCTGTTGCTGTTG3' (SEQ ID NO:51) and reverse 5'-CATAGCATCTTCATAGTCCACATC-3' (SEQ ID NO:52). Each amplification reaction underwent initial denaturation of 94°C for 30 s followed by 30 cycles of denaturation at 94°C for 5 s and annealing at 68°C for 4 min, and final extension at 72°C for 6 min.

PCR products were ligated into the pCR2.1 TOPO T/A vector (Invitrogen). Inserts were DNA-sequenced on both strands by the dideoxy chain termination method using Thermo Sequenase (Amersham Pharmacia) and an automated sequencer (Li-Cor, Lincoln, NE). Nucleotide and amino acid sequence alignment was analyzed with a DNASTAR (Madison, WI) software package, and homology searches were performed by using BLAST (Altschul, S. F. et al. (1990) J. Mol. Biol. 215, 403-410).

RNA blot analysis was subsequently performed. Northern blots (CLONTECH) were hybridized with 32P-dCTP-labeled probes: a 528-bp EcoRI fragment corresponding to the 5' untranslated (UT)-EC1 regions of the FcRH3 cDNA, a 200-bp PCR product corresponding to a portion of the 3' UT region of the FcRH2 cDNA, and a 257-bp PCR product corresponding to a portion of the 3' UT region of the FcRH1 cDNA. Membranes were hybridized for 1 h at 65°C, washed, and exposed to x-ray film (Kubagawa, H. et al. (1997) Proc. Natl. Acad. Sci. USA 94, 5261-5266).

Reverse transcription (RT)-PCR was performed. Human tonsillar cells, obtained with Institutional Review Board approval, were separated into CD19+ and CD19- subpopulations by magnetic cell sorting (Miltenyi Biotec, Auburn, CA). Viable CD19+ cells were stained with FITC-labeled anti-CD38 (Immunotech, Westbrook, ME) and phycoerythrin-labeled anti-IgD mAbs (Southern Biotechnology Associates) before sorting cells with a FACStarPlus instrument (Becton Dickinson) into Trizol reagent (Life Technologies, Grand Island, NY) for RNA isolation. Total cellular RNA was

primed with random hexamers and oligo(dT) primers and reverse-transcribed with SuperScript II (Life Technologies) into single-stranded cDNA. RT-PCR was performed by using RNA from tonsillar B cells and cell lines, with GIBCO/BRL Taq polymerase (Life Technologies). The following gene-specific primer pairs were used in the RT-PCR analysis of FcRH1-5 expression in cell lines and tonsillar B cell subpopulations:

5 FcRH1 forward, 5'-CTC AAC TTC ACA GTG CCT ACT GGG-3' (SEQ ID NO:53) and reverse, 5'-TCC TGC AGA GTC ACT AAC CTT GAG-3' (SEQ ID NO:54); FcRH2 forward, 5'-CCA GTG TAT GTC AAT GTG GGC TCT G (SEQ ID NO:55) and reverse, 5'-CAT TCT TCC CTC AAA TCT TTA CAC-3' (SEQ ID NO:56); FcRH3

10 forward, 5'-CAG CAC GTG GAT TCG AGT CAC-3' (SEQ ID NO:57) and reverse, 5'-CAG ATC TGG GAA TAA ATC GGG TTG-3' (SEQ ID NO:58) FcRH4 forward, 5'-TCT TCA GAG ATG GCG AGG TCA-3' (SEQ ID NO:59) and reverse, 5'-TTT TGG GGT GTA CAT CAA CAT ACA AG-3' (SEQ ID NO:60); and FcRH forward, 5'-TGT TGC CCT GTT TCT TCC AAT ACA-3' (SEQ ID NO:61) and reverse, 5'-CAG AGT

15 TGG CCG ACC TAC GC-3' (SEQ ID NO:62). Each amplification reaction underwent initial denaturation at 94° for 5 min followed by 35 cycles of denaturation at 94° for 30 s, annealing at 60° for 30 s, extension at 72° for 1 min, and final extension at 72° for 7 min. Amplified products were visualized in 1% agarose gels containing ethidium bromide and documented with the Bio-Rad Fluor-S Imager.

20 The following human cell lines were used: REH and Nalm 16 pro-B cell lines (Korsmeyer, S. J. et al. (1983) J. Clin. Invest. 71, 301-313); 697, 207, and OB5 pre-B cell lines (Findley, H. W. et al. (1982) Blood 60, 1305-1309; Martin, D. et al. (1991) J. Exp. Med. 173, 639-645); Ramos, Daudi, and Raji B cell lines (Pulvertaft, R. J. V. (1964) Lancet 1, 238-240; Klein, E. et al. (1968) Cancer Res. 28, 1300-1310; Klein, G.

25 et al. (1975) Intervirology 5, 319-33431-33); THP-1 and U937 monocytoid cell lines, HL-60 promyelocytic and KG-1 myelocytic cell lines, Jurkat T cell line and the K562 erythroid cell line (American Type Culture Collection).

A consensus sequence was generated that corresponds to the GenBank-derived amino terminal sequences of the second Ig-like domains of

30 FcR (FcγRI and FcγRII/III) and the third Ig-like domain of the polymeric Ig receptor:GEPIXLRCHSWKDKXLXKVITYXQNGKAXKFFH (SEQ ID NO:63). A search of the National Center for Biotechnology Information protein database with this sequence identified two overlapping human genomic bacterial artificial chromosome

(BAC) clones, AL135929 and AL356276, which are located at 1q21.2-22. The second clone contained three putative Ig superfamily genes encoding complementary amino acid sequences that were designated FcRH1, FcRH2, and FcRH3. See Figure 1. The predicted amino acid sequences of these gene segments shared 23-57% identity with each other and 14-28% identity with human FcγRI (CD64). Further analysis of the FcRH locus led to the identification of two additional genes (FcRH4, and FcRH5) and one pseudogene (FcRH4ψ), immediately centromeric of FcRH1-3, two of which have recently been described as IRTA1 (FcRH4) and IRTA2 (FcRH5) (Hatzivassiliou, G. et al. (2001) *Immunity* 14, 277-289).

To determine whether these genes are expressed by lymphocytes, the predicted amino acid sequences of their protein products were used to search the Lymphochip expressed sequence tag database with the TBLASTN algorithm (Alizadeh, A. A. et al. (2000) *Nature* (London) 403, 503-511). Two expressed sequence tags (AA505046 and AA282433) were identified that share complete identity over 23 amino acids in their translated ORFs with the N terminus of FcRH1. Lymphochip microarray data analysis indicated that these expressed sequence tags are expressed at relatively high levels in peripheral lymphoid tissues, including the lymph nodes, tonsils, resting peripheral B cells, and normal germinal center (GC) B cells. Among the different lymphoid malignancies, their expression proved to be highest in chronic lymphocytic leukemias, follicular lymphomas, and some diffuse large cell lymphomas of B lineage.

FcRH1, FcRH2, and FcRH3 cDNAs were isolated by RACE-PCR from a human lymph node cDNA library in both 5' and 3' directions. Full-length cDNAs of the coding regions for FcRH1, FcRH2, and FcRH3 were obtained by end-to-end PCR using unique primers generated from the cDNA sequences delineated for the 5' UT and 3'UT regions. Southern blot analysis of human genomic DNA digested with *Bam*HI, *Eco*RI, or *Hind*III using cDNA probes specific for the 3' UT regions of each cDNA revealed either one or two hybridizing fragments, suggesting that FcRH1, FcRH2, and FcRH3 are encoded by single genes. Analysis of full-length cDNA sequences indicated that FcRH1, FcRH2, and FcRH3 have ORFs of 1,287 bp, 1,524 bp, and 2,202 bp, respectively, and encode type I transmembrane proteins of 429 aa, 508 aa, and 734 aa, respectively. Based on predicted consensus signal peptide cleavage sites (Von Heijne, G. (1986) *Nucleic Acid Res.* 14, 4683-4690; Nielsen, H. (1997) *Protein Eng.* 10, 1-6), the relative core peptide molecular masses were estimated as 45,158 for

FcRH1, 53,407 for FcRH2, and 78,849 for FcRH3. These type I transmembrane proteins possess 3-6 extracellular C2 (Williams, A. F. & Barclay, A. N. (1988) *Annu. Rev. Immunol.* 6, 381-405; Bork, P. et al. (1994) *J. Mol. Biol.* 242, 309-320; Vaughn, D. E. & Bjorkman, P. J. (1996) *Neuron* 16, 261-273) type Ig-like domains with 3-7 potential N-linked glycosylation sites, uncharged transmembrane segments, and relatively long cytoplasmic tails containing consensus motifs for ITIMs and/or ITAMs. See Fig. 2A.

Multiple alignment analysis of the translated cDNAs, using FcRH3 as the index sequence of comparison, indicates that FcRH1, FcRH2, and FcRH3 have highly conserved hydrophobic signal peptides and corresponding Ig-like extracellular domains (Fig. 2B). Their hydrophobic transmembrane (uncharged with the exception of FcRH1 which includes an acidic domain) domains (Sonnhammer, E. L. L. et al. (1998) in *A Hidden Markov Model for Predicting Transmembrane Helices in Protein Sequences*, eds. Glasgow, J., Littlejohn, T., Major, F., Lathrop, R., Sankoff, D. & Sensen, C. (Am. Assoc. for Artificial Intelligence, Menlo Park, CA), pp. 175-182) are also well conserved, but their cytoplasmic domains are not. FcRH1 has a long cytoplasmic tail containing three potential ITAMs, the first and third of which fit the consensus sequence (E/D)-X-X-Y-X-X-(L/I)-X₆₋₈-Y-X-X-(L/I) (SEQ ID NO:64, with six amino acid between the consensus sequences; SEQ ID NO:65, with seven amino acid residues between the consensus sequences; and SEQ ID NO:66, with eight amino acid residues between the consensus sequences), whereas, the second has only one tyrosine residue. The shorter cytoplasmic domain of FcRH2 contains one potential ITAM and two ITIM consensus sequences (I/V/L/S)-X-Y-X-X-(L/V) (SEQ ID NO:67) separated by 22 amino acids. FcRH3 has the longest cytoplasmic tail. It contains one potential ITAM, one ITIM, and another potential ITAM that also has a single tyrosine residue.

An RNA blot analysis with gene-specific probes was performed on 16 human tissues, including six primary or secondary lymphoid tissues. RNA blots were analyzed with discriminating $\alpha^{32}\text{P}$ -dCTP-labeled probes generated from the respective FcRH cDNAs. The following probes were used: (Top) a PCR-generated, 257-bp probe specific to the 3' UT region of FcRH1; (Middle) a PCR-generated, 290-bp probe corresponding to the 3' UT region of FcRH2; and (Bottom) a 528-bp *EcoRI*-digested fragment of the 5' end of the FcRH3 cDNA corresponding to its 5' UT region, S1, S2, and EC1 domains. The relative mRNA abundance was indicated by β -actin probe. All

three FcRH gene probes hybridized with transcripts in the secondary lymphoid organs, spleen and lymph node. An FcRH1-specific probe hybridized with spleen and lymph node transcripts of about 3.5 kb and about 6.0 kb. Additional hybridization bands of about 0.7 kb and about 1.5 kb were observed for heart, skeletal muscle, kidney, liver, and, in less abundance, placental tissue. Larger transcripts also were seen in skeletal muscle (about 6.0 kb) and in kidney and placenta (about 4.4 kb). An FcRH2-specific probe hybridized to about 3.0-kb, about 4.4-kb, and about 5.5-kb transcripts most abundantly in spleen and lymph node. A transcript of approximately 2.4-kb was notable in the kidney. An FcRH3 probe hybridized with about 3.5-kb, about 5.5-kb, and about 7.0-kb transcripts chiefly in spleen and lymph node. These also were seen, albeit in lesser abundance, in peripheral blood lymphocytes, thymus, and bone marrow samples. Additionally, a unique transcript of about 1.35 kb was evident in skeletal muscle. These results indicated expression of FcRH1, FcRH2, and FcRH3 in peripheral lymphoid organs, whereas tissue specific differences in alternative splicing or polyadenylation were suggested by the differential expression of transcripts with variable size in nonlymphoid tissues. RTPCR analysis to date of non-lymphoid tissue skeletal muscle, however, does not reveal transcripts despite the Northern analysis results.

When FcRH expression was examined by RT-PCR analysis of cell lines representing different hematopoietic lineages, FcRH1, FcRH2, and FcRH3 expression was found in every mature B cell line tested (Table 2). FcRH2 and FcRH3 expression was limited to the mature B cell lines and not seen in the other types of cells examined. In contrast, FcRH1 expression was seen in pro-B, T, and myeloid cell lines, although not in an erythroid cell line.

Table 2. Expression of FcRH transcripts in human B cell lines

| <i>Cell Type</i> | <i>Cell line</i> | <i>FcRH1</i> | <i>FcRH2</i> | <i>FcRH3</i> |
|------------------|------------------|--------------|--------------|--------------|
| Pro-B | REH | + | - | - |
| | Nalm 16 | + | - | - |
| Pre-B | 697 | - | - | - |
| | 207 | - | - | - |
| | OB5 | - | - | - |
| B | Ramos | + | + | + |

| | | | | |
|----------------|--------|---|---|---|
| | Daudi | + | + | + |
| | Raji | + | + | + |
| T | Jurkat | + | - | - |
| Monocytic | THP-1 | + | - | - |
| Myelomonocytic | U937 | + | - | - |
| Promyelocytic | HL-60 | + | - | - |
| Myelocytic | KG-1 | + | - | - |
| Erythroid | K562 | - | - | - |

FcRH1, FcRH2, and FcRH3 expression in cell lines was determined by RT-PCR.

RT-PCR analysis of sorted populations of peripheral blood cells indicated that FcRH1, FcRH2, FcRH3, and FcRH5 are expressed at relatively high levels in CD19+ B cells, whereas FcRH4 was expressed at only trace levels. FcRH3 expression was observed in CD3+ T cells whereas transcripts of FcRH1 were barely detectable. FcRH1 expression also was observed in circulating granulocytes.

To refine the analysis of FcRH expression in secondary lymphoid tissues, tonsillar lymphocyte subpopulations were isolated. The five discrete subpopulations of B lineage cells, which can be distinguished by their differential expression of cell surface IgD and CD38, represent different stages in B cell differentiation: follicular mantle (IgD+CD38), pre-GC (IgD+CD38+), GC (IgDCD38+), memory (IgDCD38), and mature plasma cells (CD38²⁺) (Pascual, V. (1994) J. Exp. Med. 180: 329-339). RT-PCR analysis of FcRH1-5 expression in tonsillar B cell subpopulations was performed. Viable cells were magnetically sorted into CD19- non-B cells and CD19+ B cells. The latter were stained with anti-IgD and anti-CD38 mAbs, and the five subpopulations indicated (CD38- IgD-, CD38- IgD+, CD38+ IgD+, CD38+ IgD-, and CD38²⁺) were sorted by flow cytometry. RT-PCR analysis of FcRH transcripts in non-B cells and the B cell subpopulations was also performed. After cDNA preparation, PCR amplification was performed on the equivalent template of approximately 10 k cells. Glyceraldehyde-3-phosphate dehydrogenase (GADPH) was amplified as a positive control.

RT-PCR analysis indicated little or no expression of FcRH transcripts in the non-B lineage CD19- cells, most of which are T cells. However, CD19+ subpopulations displayed coordinate expression of FcRH1, FcRH2, and FcRH3 transcripts in follicular

mantle, naïve, GC, and memory B cell subpopulations, but yielded no evidence of FcRH transcripts in pre-GC B cells or plasma cells. In contrast, FcRH4 transcripts were restricted to the follicular mantle and memory B cells, whereas FcRH5 expression extended to mature plasma cells.

5 The relationship between the five FcRHs was examined by comparing their full-length, extracellular, and individual Ig-like domain amino acid sequences. This analysis, which included a recently identified mouse FcRH ortholog (moFcRH) and members of the FcR family, used the CLUSTAL method algorithm (Higgins, D. G. & Sharp, P. M. (1989) *Comput. Appl. Biosci.* 5, 151-153). Comparison of the full-length
10 sequences of other FcRH family members with FcRH3 indicated 40-47% identity. By comparison, the degree of FcRH3 homology with the moFcRH was found to be 35% and 21-24% with FcR members residing on chromosome 1, FcγRI, FcγRII, FcγRIII, and FcεRI. A lower level of amino acid identity (14%) was observed for the chromosome
15 19 LRC member, FcαR. A slightly higher degree of extracellular homology was evident. Pairwise analysis of the individual Ig-like subunits indicated conservation in membrane-distal to membrane-proximal ordering of extracellular domain composition among family members. Although similar Ig domain subunits were shared among family members, the individual receptors were found to be composed of unique domain combinations. The extracellular domain configuration of the moFcRH most closely
20 resembled that of FcRH2, with which it has 46% identity. The extended pairwise comparison of the FcRH family with known FcRs suggested the conservation of these Ig-like domains to some degree throughout the greater family. The resemblance is particularly evident in the FcRH3 membrane-distal domains that correspond to the three FcγRI domains and the two domains of FcγRII, FcγRIII, and the FcR γ-chain. This
25 analysis suggests the ancestral occurrence of differential duplication and diversification of the individual Ig-like subunits in the respective FcRH family members. The data also indicate that the FcRHs are more similar to their FcR neighbors on chromosome 1 than to their FcR relative on chromosome 19.

 The genomic sequence analysis of relevant chromosome 1q21 BAC
30 clones indicated that the entire FcRH locus spans 300 kb. The FcRH genes lie in the same transcriptional orientation toward the centomere. Exon-intron boundaries were characterized by sequence comparison of their respective cDNA clones and the AG/GT rule. The FcRH1 gene consists of 11 exons and 10 introns spanning about 28 kb. The

first exon, 5' UT/S1, encodes the 5' UT region, the ATG translation initiation codon, and the first half of a split signal peptide. S2, the second exon, is separated from 5' UT/S1 by a long intron of 12.9 kb and, like the neighboring FcRs, is 21 bp in length (van de Winkel, J. G. & Capel, P. J. (1993) *Immunol. Today* 14, 215-221; Kulczycki, A., Jr. et al. (1990) *Proc. Natl. Acad. Sci. USA* 87, 2856-2860; Pang, J. et al. (1994) *J. Immunol.* 151, 6166-6174.). The extracellular region is encoded by three closely clustered exons, EC1-EC3, that code for the three Ig-like domains. The membrane-proximal, transmembrane, and the proximal portion of the cytoplasmic domain are encoded by a single sixth exon, TM. The cytoplasmic tail is encoded by five exons, CY1-CY5, and the CY5 also encodes the beginning of the 3' UT region.

FcRH2 contains 12 exons and 11 introns that span 30 kb. It also contains two exons that encode a split signal peptide, the first of which, 5'UT/S1, includes the 5' UT region, the ATG translation initiation codon, and first half of the signal peptide. The second exon, S2, is 21 bp in length. Exons 3-6 encode the four extracellular domains, EC1-EC4. The seventh exon encodes the membrane-proximal, transmembrane, and the proximal portion of the cytoplasmic domain. The FcRH2 cytoplasmic tail is encoded by five exons, CY1-CY5, the last exon of which includes the termination of the ORF and beginning of the 3' UT region.

The FcRH3 gene consists of 16 exons and 15 introns that span about 24 kb. Unlike FcRH1 and FcRH2, its 5' UT region is encoded by two exons, 5' UT1 and a second, 5'UT2/S1, that also encodes the ATG translation initiation codon and the beginning of the split signal peptide. The third exon, S2, is also 21 bp in length. Extracellular domains encoded by six exons, EC1-EC6, are followed by exon 10 that encodes the membrane-proximal, transmembrane, and the proximal portion of the cytoplasmic domain. The cytoplasmic tail is encoded by five exons, CY1-CY5; the last contains the beginning of the 3' UT region.

Identification of HuFcRH6

FcRH6 is located in the midst of the classical FcRs at 1q21-23. Its genomic structure indicates, like the classical FcRs and FcRH1-5, a split hydrophobic signal peptide encoded by two exons the second of which is 21bp.

5 FcRH6 was characterized using the methods described in Example 1. A composite analysis of Ig-like domains for relatedness with the other huFcRHs was performed. See Figure xxx. Sequence analysis of huFcRH6 indicates its type I transmembrane form contains a consensus motif for a single ITAM, or a single or two ITIM's.

10 Initial RT-PCR analysis of huFcRH6 in human tissues and cell lines (as described in Example 1) reveals transcript expression in normal tonsil and lymph nodes. In cell lines, expression of huFcRH6 was identified in myeloid cell lines THP-1 (monocytic), U937 (myelomonocytic), and KG-1 (myelocytic). Limited expression if any was identified in the 207 pre-B cell line and the Daudi B cell line.

15

EXAMPLE 3

Generation of Transfectants and Antibodies

Recombinant constructs for transfection and stable expression of huFcRH1-5 have been generated. The constructs have been ligated into a CMV driven mammalian
20 expression vector with and without green fluorescent protein (GFP) fusion at the carboxyl terminus. Surface expression of huFcRH1 and huFcRH3 was detected for both GFP and non-GFP forms by staining with antibody supernatant. The antibody supernatant was derived from hybridomas generated by mice immunized with recombinant extracellular protein of the respective FcRH. The constructs for huFcRH2,
25 4, and 5 have been detected by green fluorescence as well as surface expression for FcRH4.

Monoclonal antibodies have been generated, including, for example, an antibody that binds FcRH1. The preliminary analysis of FACS staining for FcRH1
30 expression with monoclonal antibody 1-5A3 labeled with a FITC conjugate (mouse anti human FcRH1) in peripheral blood from normal volunteers indicates virtually all CD19+ B cells have huFcRH1 expression, as do CD14+ monocytes and CD13+ granulocytes. CD3+ T cells have limited to no expression of FcRH1. Staining of B-CLL samples from two different patient peripheral blood samples indicates that virtually all

CD5+/CD19+ B-CLL cells are positive for the FcRH1 1-5A3 antigen. By western blot analysis of recombinant protein for FcRH1-5 extracellular regions 1-5A3 appears specific for FcRH1. 1-5A3 also stains B cell lines Daudi and Raji.

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EXAMPLE 4

Identification of MoFcRH1-3

A family of three mouse Fc Receptor Homologs (MoFCRHs) were identified and cloned. Amino acid sequences from the membrane proximal Ig-like domains of huFcRH1-5 were used to identify putative mouse FcRH orthologs in the NCBI or
10 Celera genomic, EST, and protein databases using the protein BLAST (BLASTP) and the translated nucleotide BLAST (TBLASTN) algorithms, respectively. The location of moFcR family is split between chromosomes 1 and 3 in regions syntenic with human chromosome 1q21-23. See Figure 4. The mo FcRH are located on mouse Ch3. Approximate positions were determined from Genbank, Celera, and Mouse
15 Genome Informatics databases. Contigs of ESTs were generated to determine the putative cDNA sequences.

Genomic organization was determined by comparing cDNA clones generated from RACE PCR with GenBank and Celera genomic sequences. DNASTar software was used for analysis of exon-intron boundaries which were characterized by sequence
20 comparison and the AG/GT rule. All three genes contain a split signal sequence with a 21bp S2 exon (exon 2) which is found in all FcR and huFcRH genes on human chromosome 1.

A comparison of tyrosine based motifs in FcRH cytoplasmic tails indicated homology with the huFcRH family. See Figure 5. An analysis of sequence homology
25 conservation is further shown in Figures 6 and 7.

Expression of the moFcRHs in tissue and cell lines was also characterized as described in Example 1. Briefly, RT-PCR was performed on mouse tissues and cell lines with gene specific primers. Viable tissue was placed in TRIzol reagent for RNA extraction. After cDNA preparation PCT amplification was performed on equivalent
30 template amounts. Actin was amplified as a positive control. McFcRH3 appears to have preferential expression in cells of B lineage. The results are shown in Tables 3-4.

Table 3: Tissue Distribution of moFcRH Expression

| TISSUE | MoFcRH1 | MoFcRH2 | MoFcRH3 |
|------------------|---------|---------|---------|
| Bone Marrow | + | + | + |
| Thymus | + | + | + |
| Spleen | + | + | + |
| Lymph Node | + | + | + |
| Peyer's Patches | + | + | + |
| Peripheral Blood | + | + | + |
| Brain | + | - | - |
| Liver | + | + | - |
| Heart | + | - | - |
| Muscle | + | - | - |
| Kidney | + | - | - |
| Lung | + | + | - |
| Intestine | + | + | + |
| Testes | + | - | - |

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Table 4. Expression of moFcRH transcripts in cell lines

| <i>Cell Type</i> | <i>Cell line</i> | <i>FcRH1</i> | <i>FcRH2</i> | <i>FcRH3</i> |
|------------------|------------------|--------------|--------------|--------------|
| Pro-B | SCID7 | + | +/- | + |
| | Raw8.1 | + | + | - |
| Pre-B | 70Z/3 | + | + | + |
| | BC76 | - | + | + |
| | 18-81 | + | + | + |
| Imm. B | WEHI-231 | + | + | + |
| | WEHI-279 | + | + | + |
| B | A20 | + | + | + |
| | X16C8.5 | + | + | + |
| T | EL4 | + | +/- | -/+ |
| NKT | NKT | + | +/- | - |
| NKT | 2C12 | + | +/- | - |
| Myeloid | WEHI-3 | + | - | - |
| Lymphoid | YAC-1 | + | + | - |
| Fibroblast | 3T3 | + | +/- | - |

Expression in cell lines was determined by RT-PCR.

- 5 The mouse FcReceptor Homologs include secreted or type I transmembrane isoforms that have unique cytoplasmic tails with potential activation and inhibition motifs. Their chromosomal location, Ig domain homology, and genomic organization indicate the mouse FcReceptor Homologs are orthologs of the huFcRH that have evolved a significant level of diversity. moFcRH1, moFcRH2, and moFcRH3 are
- 10 predicted to encode secreted or type I transmembrane proteins based on their amino acid sequences. moFcRH1 has two secreted isoforms both of which have extracellular (EC) regions of four Ig-like domains with five potential sites for N-linked glycosylation. One isoform is a fusion protein with a type B scavenger receptor domain containing 8 cysteines. moFcRH2 has secreted and type I isoforms containing two Ig-
- 15 like domains with five N-linked glycosylation sites. The type I isoform has an uncharged transmembrane region which the secreted isoform lacks. Both isoforms

contain the cytoplasmic portion which is long in the transmembrane form and contains five tyrosines including a consensus sequence for one potential immunoreceptor tyrosine-based activating motif . moFcRH3 contains five Ig-like domains with six potential sites of N-linked glycosylation. Its transmembrane domain is also uncharged
5 and the cytoplasmic region contains one potential ITAM and one potential immunoreceptor tyrosine-based inhibitory motif. The amino acid (aa) length of individual regions and full length (FL) isoforms, as well as approximate molecular weight (MW) in Daltons (Da), is indicated in the structural diagram of Figure 8.

Throughout this application, various publications are referenced. The
10 disclosures of these publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

It will be apparent to those skilled in the art that various modifications and variations can be made in the present invention without departing from the scope or
15 spirit of the invention. Other embodiments of the invention will be apparent to those skilled in the art from consideration of the specification and practice of the invention disclosed herein. It is intended that the specification and examples be considered as exemplary only, with a true scope and spirit of the invention being indicated by the following claims.

20

What is claimed is:

1. An isolated FcRH, comprising a cytoplasmic region with more than 107 or less than 104 amino acids, a transmembrane region, and an extracellular region.
2. The isolated FcRH of claim 1, wherein the extracellular region comprises less than four Ig domains.
3. The isolated FcRH of claim 2, wherein the cytoplasmic region comprises less than 104 amino acids.
4. The isolated FcRH of claim 3, wherein the transmembrane region comprises an acidic amino acid.
5. The isolated FcRH of claim 4, wherein the acidic amino acid is glutamate.
6. The isolated FcRH of claim 2, wherein the cytoplasmic region comprises the amino acid sequence of SEQ ID NO:1
7. The isolated FcRH of claim 2, wherein the extracellular region comprises the amino acid sequence of SEQ ID NO:21.
8. The isolated FcRH of claim 1, comprising the amino acid sequence of SEQ ID NO:2.
9. The isolated FcRH of claim 1, wherein the receptor is expressed by myeloid cells.
10. The isolated FcRH of claim 9, wherein the receptor is expressed by T-cells.
11. A polypeptide comprising the amino acid sequence of SEQ ID NO:1.
12. A polypeptide comprising the amino acid of SEQ ID NO:1 with conservative amino acid substitutions.
13. A polypeptide comprising the amino acid sequence of SEQ ID NO:21
14. A polypeptide comprising the amino acid of SEQ ID NO:21 with conservative amino acid substitutions.
15. A polypeptide comprising the amino acid of SEQ ID NO:2.
16. A polypeptide comprising the amino acid of SEQ ID NO:2 with conservative amino acid substitutions.
17. The isolated FcRH of claim 1, wherein the cytoplasmic region comprises less than 99 amino acids and wherein the receptor further comprises an extracellular region with up to four Ig domain and up to five N-linked glycosylation sites.

18. The isolated FcRH of claim 17, wherein the cytoplasmic region comprises the amino acid sequence of SEQ ID NO:3.
19. The isolated FcRH of claim 17, wherein the extracellular region comprises the amino acid sequence of SEQ ID NO:22.
20. The isolated FcRH of claim 1, comprising the amino acid sequence of SEQ ID NO:4.
21. A polypeptide comprising the amino acid sequence of SEQ ID NO:3.
22. A polypeptide comprising the amino acid of SEQ ID NO:3 with conservative amino acid substitutions.
23. A polypeptide comprising the amino acid sequence of SEQ ID NO:22
24. A polypeptide comprising the amino acid of SEQ ID NO:22 with conservative amino acid substitutions.
25. A polypeptide comprising the amino acid of SEQ ID NO:4.
26. A polypeptide comprising the amino acid of SEQ ID NO:4 with conservative amino acid substitutions.
27. The isolated FcRH of claim 1, wherein the cytoplasmic region comprises more than 107 amino acids.
28. The isolated FcRH of claim 27, wherein the cytoplasmic region comprises the amino acid sequence of SEQ ID NO:5.
29. The isolated FcRH of claim 27, wherein the cytoplasmic region comprises the amino acid sequence of SEQ ID NO:23.
30. The isolated FcRH of claim 27, wherein the extracellular region comprises the amino acid sequence of SEQ ID NO:24.
31. The isolated FcRH of claim 1, comprising the amino acid sequence of SEQ ID NO:6.
32. The isolated FcRH of claim 1, comprising the amino acid sequence of SEQ ID NO:25.
33. A polypeptide comprising the amino acid sequence of SEQ ID NO:5
34. A polypeptide comprising the amino acid of SEQ ID NO:5 with conservative amino acid substitutions.
35. A polypeptide comprising the amino acid sequence of SEQ ID NO:24
36. A polypeptide comprising the amino acid of SEQ ID NO:24 with conservative amino acid substitutions.

37. A polypeptide comprising the amino acid sequence of SEQ ID NO:23
38. A polypeptide comprising the amino acid of SEQ ID NO:23 with conservative amino acid substitutions.
39. A polypeptide comprising the amino acid sequence of SEQ ID NO:6.
40. A polypeptide comprising the amino acid of SEQ ID NO:6 with conservative amino acid substitutions.
41. A polypeptide comprising the amino acid sequence of SEQ ID NO:25.
42. A polypeptide comprising the amino acid of SEQ ID NO:25 with conservative amino acid substitutions.
43. The isolated FcRH of claim 1, wherein the cytoplasmic region comprises the amino acid sequence of SEQ ID NO:26.
44. The isolated FcRH of claim 1, wherein the extracellular region comprises the amino acid sequence of SEQ ID NO:27.
45. The isolated FcRH of claim 1, comprising the amino acid sequence of SEQ ID NO:28.
46. An isolated nucleic acid, comprising a nucleotide sequence that encodes the FcRH of claim 2.
47. An isolated nucleic acid, comprising a nucleotide sequence that encodes SEQ ID NO:1.
48. An isolated nucleic acid, comprising a nucleotide sequence that encodes SEQ ID NO:21.
49. An isolated nucleic acid, comprising a nucleotide sequence that encodes SEQ ID NO:2.
50. The nucleic acid of claim 46, comprising the nucleotide sequence of SEQ ID NO:7.
51. An isolated nucleic acid comprising a sequence that hybridizes under highly stringent conditions to a hybridization probe, wherein the hybridization probe comprises the nucleotide sequence of SEQ ID NO:7, or the complement of SEQ ID NO:7.
52. The nucleic acid of claim 46, comprising the nucleotide sequence of SEQ ID NO:13.
53. An isolated nucleic acid comprising a sequence that hybridizes under highly stringent conditions to a hybridization probe, wherein the hybridization probe

comprises the nucleotide sequence of SEQ ID NO:13 or the complement of SEQ ID NO:13.

54. The nucleic acid of claim 46, comprising the nucleotide sequence of SEQ ID NO:8.
55. An isolated nucleic acid comprising a sequence that hybridizes under highly stringent conditions to a hybridization probe, wherein the hybridization probe comprises the nucleotide sequence of SEQ ID NO:8, or the complement of SEQ ID NO:8.
56. A single stranded nucleic acid that hybridizes under stringent conditions to a nucleic acid having the sequence of SEQ ID NO:7, SEQ ID NO:13 or SEQ ID NO:8.
57. An isolated nucleic acid, comprising a nucleotide sequence that encodes the FcRH of claim 17.
58. An isolated nucleic acid, comprising a nucleotide sequence that encodes SEQ ID NO:3.
59. An isolated nucleic acid, comprising a nucleotide sequence that encodes SEQ ID NO:22.
60. An isolated nucleic acid, comprising a nucleotide sequence that encodes SEQ ID NO:4.
61. The nucleic acid of claim 57, comprising the nucleotide sequence of SEQ ID NO:9.
62. An isolated nucleic acid comprising a sequence that hybridizes under highly stringent conditions to a hybridization probe, wherein the hybridization probe comprises the nucleotide sequence of SEQ ID NO:9, or the complement of SEQ ID NO:9.
63. The nucleic acid of claim 57, comprising the nucleotide sequence of SEQ ID NO:14.
64. An isolated nucleic acid comprising a sequence that hybridizes under highly stringent conditions to a hybridization probe, wherein the hybridization probe comprises the nucleotide sequence of SEQ ID NO:14, or the complement of SEQ ID NO:14.
65. The nucleic acid of claim 57, comprising the nucleotide sequence of SEQ ID NO:10.

66. An isolated nucleic acid comprising a sequence that hybridizes under highly stringent conditions to a hybridization probe, wherein the hybridization probe comprises the nucleotide sequence of SEQ ID NO:10, or the complement of SEQ ID NO:10.
67. A single stranded nucleic acid that hybridizes under stringent conditions to a nucleic acid having the sequence of SEQ ID NO:9, SEQ ID NO:14, or SEQ ID NO:10.
68. An isolated nucleic acid, comprising a nucleotide sequence that encodes the FcRH of claim 27.
69. An isolated nucleic acid, comprising a nucleotide sequence that encodes SEQ ID NO:5.
70. An isolated nucleic acid, comprising a nucleotide sequence that encodes SEQ ID NO:23.
71. An isolated nucleic acid, comprising a nucleotide sequence that encodes SEQ ID NO:24.
72. An isolated nucleic acid, comprising a nucleotide sequence that encodes SEQ ID NO:6.
73. An isolated nucleic acid, comprising a nucleotide sequence that encodes SEQ ID NO:25.
74. The nucleic acid of claim 68, comprising the nucleotide sequence of SEQ ID NO:11.
75. An isolated nucleic acid comprising a sequence that hybridizes under highly stringent conditions to a hybridization probe, wherein the hybridization probe comprises the nucleotide sequence of SEQ ID NO:11, or the complement of SEQ ID NO:11.
76. The nucleic acid of claim 68, comprising the nucleotide sequence of SEQ ID NO:16.
77. An isolated nucleic acid comprising a sequence that hybridizes under highly stringent conditions to a hybridization probe, wherein the hybridization probe comprises the nucleotide sequence of SEQ ID NO:16, or the complement of SEQ ID NO:16.
78. The nucleic acid of claim 68, comprising the nucleotide sequence of SEQ ID NO:15.

79. An isolated nucleic acid comprising a sequence that hybridizes under highly stringent conditions to a hybridization probe, wherein the hybridization probe comprises the nucleotide sequence of SEQ ID NO:15, or the complement of SEQ ID NO:15.
80. The nucleic acid of claim 68, comprising the nucleotide sequence of SEQ ID NO:12.
81. An isolated nucleic acid comprising a sequence that hybridizes under highly stringent conditions to a hybridization probe, wherein the hybridization probe comprises the nucleotide sequence of SEQ ID NO:12, or the complement of SEQ ID NO:12.
82. The nucleic acid of claim 68, comprising the nucleotide sequence of SEQ ID NO:17.
83. An isolated nucleic acid comprising a sequence that hybridizes under highly stringent conditions to a hybridization probe, wherein the hybridization probe comprises the nucleotide sequence of SEQ ID NO:11, or the complement of SEQ ID NO:17.
84. A single stranded nucleic acid that hybridizes under stringent conditions to a nucleic acid having the sequence of SEQ ID NO:11, SEQ ID NO:15, SEQ ID NO:16, or SEQ ID NO:12.
85. An isolated nucleic acid, comprising a nucleotide sequence that encodes SEQ ID NO:26.
86. An isolated nucleic acid, comprising a nucleotide sequence that encodes SEQ ID NO:27.
87. An isolated nucleic acid, comprising a nucleotide sequence that encodes SEQ ID NO:28.
88. An isolated nucleic acid comprising a sequence that hybridizes under highly stringent conditions to a hybridization probe, wherein the hybridization probe comprises the nucleotide sequence of SEQ ID NO:18, or the complement of SEQ ID NO:18.
89. An isolated nucleic acid comprising a sequence that hybridizes under highly stringent conditions to a hybridization probe, wherein the hybridization probe comprises the nucleotide sequence of SEQ ID NO:19, or the complement of SEQ ID NO:19.

90. An isolated nucleic acid comprising a sequence that hybridizes under highly stringent conditions to a hybridization probe, wherein the hybridization probe comprises the nucleotide sequence of SEQ ID NO:20, or the complement of SEQ ID NO:20.
91. A single stranded nucleic acid that hybridizes under stringent conditions to a nucleic acid having the sequence of SEQ ID NO:18, SEQ ID NO:19, or SEQ ID NO:20.
92. An expression vector comprising the nucleic acid of claim 46 operably linked to an expression control sequence.
93. An isolated cell comprising the vector of claim 92.
94. A method of making a FcRH, comprising culturing the cell of claim 93 under conditions permitting expression of the FcRH.
95. An expression vector comprising the nucleic acid of claim 57 operably linked to an expression control sequence.
96. An isolated cell comprising the vector of claim 95.
97. A method of making a FcRH, comprising culturing the cell of claim 96 under conditions permitting expression of the FcRH.
98. An expression vector comprising the nucleic acid of claim 56 operably linked to an expression control sequence.
99. An isolated cell comprising the vector of claim 98.
100. A method of making a FcRH, comprising culturing the cell of claim 99 under conditions permitting expression of the FcRH.
101. An expression vector comprising the nucleic acid of claim 57 operably linked to an expression control sequence.
102. An isolated cell comprising the vector of claim 101.
103. A method of making a FcRH, comprising culturing the cell of claim 102 under conditions permitting expression of the FcRH.
104. An expression vector comprising the nucleic acid of claim 67 operably linked to an expression control sequence.
105. An isolated cell comprising the vector of claim 104.
106. A method of making a FcRH, comprising culturing the cell of claim 105 under conditions permitting expression of the FcRH.

107. An expression vector comprising the nucleic acid of claim 68 operably linked to an expression control sequence.
108. An isolated cell comprising the vector of claim 107.
109. A method of making a FcRH, comprising culturing the cell of claim 108 under conditions permitting expression of the FcRH.
110. An expression vector comprising the nucleic acid of claim 91 operably linked to an expression control sequence.
111. An isolated cell comprising the vector of claim 110.
112. A method of making a FcRH, comprising culturing the cell of claim 111 under conditions permitting expression of the FcRH.
113. A purified antibody or immunonologic fragment thereof, wherein the antibody or fragment thereof selectively binds to the FcRH of claim 1.
114. A purified antibody or immunonologic fragment thereof, wherein the antibody or fragment thereof selectively binds to the FcRH of claim 2.
115. A purified antibody or immunonologic fragment thereof, wherein the antibody or fragment thereof selectively binds to the FcRH of claim 17.
116. A purified antibody or immunonologic fragment thereof, wherein the antibody or fragment thereof selectively binds to the FcRH of claim 27.
117. The antibody or fragment of claim 113, wherein the antibody or fragment is a monoclonal antibody or fragment thereof.
118. The antibody or fragment of claim 113, wherein the antibody or fragment thereof is a humanized antibody, a fully human antibody, or a fragment thereof.
119. The antibody or fragment of claim 113, wherein the antibody or fragment thereof is a single chain antibody or fragment thereof.
120. The antibody or fragment of claim 113, wherein the antibody or fragment thereof is labeled.
121. The antibody or fragment of claim 113, wherein the label is a radiolabel.
122. The antibody or fragment of claim 113, wherein the antibody or fragment is conjugated or fused with a toxin.
123. A purified antibody that selectively binds to the FcRH of claim 6, but not to the FcRH of claim 18, 28, or 43.
124. A purified antibody that selectively binds to the FcRH of claim 18, but not to the FcRH of claim 6, 28, or 43.

125. A purified antibody that selectively binds to the FcRH of claim 28, but not to the FcRH of claim 6, 18, or 43.
126. The purified antibody of claim 125, wherein the antibody does not bind to the FcRH of claim 29.
127. A purified antibody that selectively binds to the FcRH of claim 29, but not to the FcRH of claim 6, 18, or 43.
128. The purified antibody of claim 127, wherein the antibody does not bind to the FcRH of claim 28.
129. A purified antibody that selectively binds to the FcRH of claim 43, but not to the FcRH of claim 6, 18, or 28.
130. A purified antibody that selectively binds to the FcRH of claim 7, but not to the FcRH of claim 19, 30, or 44.
131. A purified antibody that selectively binds to the FcRH of claim 19, but not to the FcRH of claim 7, 30, or 44.
132. A purified antibody that selectively binds to the FcRH of claim 30, but not to the FcRH of claim 7, 19, or 44.
133. A purified antibody that selectively binds to the FcRH of claim 44, but not to the FcRH of claim 7, 19, or 30.
134. A method of diagnosing a malignancy of hematopoietic cell lineage in a subject, comprising:
 - (a) contacting a biological sample of the subject with the antibody of claim 113 under conditions that allow the antibody to bind to an FcRH in the biological sample;
 - (b) detecting the amount or pattern of binding by the antibody, changes in the amount or pattern of binding as compared to binding in a control sample indicating a malignancy of hematopoietic cell lineage in the subject.
135. The method of claim 134, wherein the malignancy of hematopoietic cell lineage is a malignancy of B cell lineage.
136. The method of claim 134, wherein the malignancy of hematopoietic cell lineage is a malignancy of T cell lineage.
137. The method of claim 134, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:1.

138. The method of claim 134, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:21.
139. The method of claim 134, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:2.
140. The method of claim 134, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:3.
141. The method of claim 134, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:22.
142. The method of claim 134, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:4.
143. The method of claim 134, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:5.
144. The method of claim 134, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:23.
145. The method of claim 134, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:24.
146. The method of claim 134, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:6.
147. The method of claim 134, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:25.
148. The method of claim 134, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:26.
149. The method of claim 134, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:27.
150. The method of claim 134, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:28.
151. A method of diagnosing a malignancy of hematopoietic cell lineage in a subject, comprising:
 - (a) contacting the nucleic acid of claim 56 with a biological sample of the subject under conditions that allow the nucleic acid to hybridize with an FcRH in the biological sample;

- (b) detecting the amount or pattern of binding by the nucleic acid, changes in the amount or pattern of binding as compared to binding in a control sample indicating a malignancy of hematopoietic cell lineage in the subject.
152. The method of claim 151, wherein the malignancy of hematopoietic cell lineage is a malignancy of B cell lineage.
153. The method of claim 151, wherein the malignancy of hematopoietic cell lineage is a malignancy of T cell lineage.
154. A method of diagnosing a malignancy of hematopoietic cell lineage in a subject, comprising:
- (a) contacting the nucleic acid of claim 67 with a biological sample of the subject under conditions that allow the nucleic acid to hybridize with the biological sample;
 - (b) detecting the amount or pattern of binding by the nucleic acid, changes in the amount or pattern of binding as compared to binding in a control sample indicating a malignancy of hematopoietic cell lineage.
155. The method of claim 154, wherein the malignancy of hematopoietic cell lineage is a malignancy of B cell lineage.
156. The method of claim 154, wherein the malignancy of hematopoietic cell lineage is a malignancy of T cell lineage.
157. A method of diagnosing a malignancy of hematopoietic cell lineage in a subject, comprising:
- (a) contacting the nucleic acid of claim 84 with a biological sample of the subject under conditions that allow the nucleic acid to hybridize with the biological sample;
 - (b) detecting the amount or pattern of binding by the nucleic acid, changes in the amount or pattern of binding as compared to binding in a control sample indicating a malignancy of hematopoietic cell lineage.
158. The method of claim 157, wherein the malignancy of hematopoietic cell lineage is a malignancy of B cell lineage.
159. The method of claim 157, wherein the malignancy of hematopoietic cell lineage is a malignancy of T cell lineage.

160. A method of diagnosing a malignancy of hematopoietic cell lineage in a subject, comprising:
- (a) contacting the nucleic acid of claim 91 with a biological sample of the subject under conditions that allow the nucleic acid to hybridize with the biological sample;
 - (b) detecting the amount or pattern of binding by the nucleic acid, changes in the amount or pattern of binding as compared to binding in a control sample indicating a malignancy of hematopoietic cell lineage.
161. The method of claim 160, wherein the malignancy of hematopoietic cell lineage is a malignancy of B cell lineage.
162. The method of claim 160, wherein the malignancy of hematopoietic cell lineage is a malignancy of T cell lineage.
163. A method of treating a malignancy of hematopoietic cell lineage in a subject, comprising contacting the subject's malignant cells with a therapeutically effective amount of the antibody of claim 113.
164. The method of claim 163, wherein the malignancy of hematopoietic cell lineage is a malignancy of B cell lineage.
165. The method of claim 163, wherein the malignancy of hematopoietic cell lineage is a malignancy of T cell lineage.
166. The method of claim 163, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:1.
167. The method of claim 163, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:21.
168. The method of claim 163, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:2.
169. The method of claim 163, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:3.
170. The method of claim 163, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:22.
171. The method of claim 163, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:4.
172. The method of claim 163, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:5.

173. The method of claim 163, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:23.
174. The method of claim 163, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:24.
175. The method of claim 163, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:6.
176. The method of claim 163, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:25.
177. The method of claim 163, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:26.
178. The method of claim 163, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:27.
179. The method of claim 163, wherein the antibody selectively binds an FcRH having the amino acid sequence of SEQ ID NO:28.
180. A method of treating a malignancy of hematopoietic cell lineage in a subject, comprising contacting the subject's malignant cells with a therapeutically effective amount of the nucleic acid of claim 56.
181. A method of treating a malignancy of hematopoietic cell lineage in a subject, comprising contacting the subject's malignant cells with a therapeutically effective amount of the nucleic acid of claim 67.
182. A method of treating a malignancy of hematopoietic cell lineage in a subject, comprising contacting the subject's malignant cells with a therapeutically effective amount of the nucleic acid of claim 84.
183. A method of treating a malignancy of hematopoietic cell lineage in a subject, comprising contacting the subject's malignant cells with a therapeutically effective amount of the nucleic acid of claim 91.
184. A method of diagnosing an autoimmune disease in a subject, comprising:
 - (a) contacting a biological sample of the subject with the antibody of claim 113 under conditions that allow the antibody to bind to FcRH in the biological sample;
 - (b) detecting the amount or pattern of binding by the antibody, changes in the amount or pattern of binding as compared to binding in a control sample indicating an autoimmune disease in the subject.

185. A method of diagnosing an autoimmune disease in a subject, comprising:
- (a) contacting the nucleic acid of claim 56 with a biological sample of the subject under conditions that allow the nucleic acid to hybridize with the biological sample;
 - (b) detecting the amount or pattern of binding by the nucleic acid, changes in the amount or pattern of binding as compared to binding in a control sample indicating an autoimmune disease.
186. A method of diagnosing an autoimmune disease in a subject, comprising:
- (a) contacting the nucleic acid of claim 67 with a biological sample of the subject under conditions that allow the nucleic acid to hybridize with the biological sample;
 - (b) detecting the amount or pattern of binding by the nucleic acid, changes in the amount or pattern of binding as compared to binding in a control sample indicating an autoimmune disease.
187. A method of diagnosing an autoimmune disease in a subject, comprising:
- (a) contacting the nucleic acid of claim 84 with a biological sample of the subject under conditions that allow the nucleic acid to hybridize with the biological sample;
 - (b) detecting the amount or pattern of binding by the nucleic acid, changes in the amount or pattern of binding as compared to binding in a control sample indicating an autoimmune disease.
188. A method of diagnosing an autoimmune disease in a subject, comprising:
- (a) contacting the nucleic acid of claim 91 with a biological sample of the subject under conditions that allow the nucleic acid to hybridize with the biological sample;
 - (b) detecting the amount or pattern of binding by the nucleic acid, changes in the amount or pattern of binding as compared to binding in a control sample indicating an autoimmune disease.
189. A method of treating an autoimmune disease in a subject, comprising contacting, with a therapeutically effective amount of the antibody of claim 113, one or more FcRH expressing cells of the subject.
190. A method of treating an autoimmune disease in a subject, comprising contacting, with a therapeutically effective amount of the nucleic acid of claim 56,

FcRH expressing cells of the subject.

191. A method of treating an autoimmune disease in a subject, comprising contacting, with a therapeutically effective amount of the nucleic acid of claim 67, FcRH expressing cells of the subject.
192. A method of treating an autoimmune disease in a subject, comprising contacting, with a therapeutically effective amount of the nucleic acid of claim 84, FcRH expressing cells of the subject.
193. A method of treating an autoimmune disease in a subject, comprising contacting, with a therapeutically effective amount of the nucleic acid of claim 91, FcRH expressing cells of the subject.
194. A method of modulating a humoral immune response in a subject, comprising administering to the subject the isolated FcRH of claim 1.
195. A method of modulating a humoral immune response in a subject, comprising administering to the subject the antibody of claim 113.
196. A method of modulating a humoral immune response in a subject, comprising administering to the subject the nucleic acid of claim 56.
197. A method of modulating a humoral immune response in a subject, comprising administering to the subject the nucleic acid of claim 67.
198. A method of modulating a humoral immune response in a subject, comprising administering to the subject the nucleic acid of claim 84.
199. A method of modulating a humoral immune response in a subject, comprising administering to the subject the nucleic acid of claim 91.
200. An isolated mouse FcRH isoform of FcRH1, wherein the isoform lacks a cytoplasmic region.
201. A polypeptide comprising the amino acid sequence of SEQ ID NO:70.
202. A polypeptide comprising the amino acid of SEQ ID NO:70 with conservative amino acid substitutions.
203. An isolated mouse FcRH isoform of FcRH2, wherein the FcRH lacks a transmembrane region.
204. A polypeptide comprising the amino acid sequence of SEQ ID NO:73.
205. A polypeptide comprising the amino acid of SEQ ID NO:73 with conservative amino acid substitutions.
206. A polypeptide comprising the amino acid of SEQ ID NO:77.

207. A polypeptide comprising the amino acid of SEQ ID NO:77 with conservative amino acid substitutions.
208. A polypeptide comprising the amino acid sequence of SEQ ID NO:78.
209. A polypeptide comprising the amino acid sequence of SEQ ID NO:78 with conservative amino acid substitutions.
210. A nucleic acid encoding the isolated mouse FcRH isoform of claim 200.
211. A nucleic acid encoding the isolated mouse FcRH isoform of claim 203.
212. A nucleic acid encoding the polypeptide of claim 201.
213. A nucleic acid encoding the polypeptide of claim 202.
214. A nucleic acid encoding the polypeptide of claim 204.
215. A nucleic acid encoding the polypeptide of claim 205.
216. A nucleic acid encoding the polypeptide of claim 206.
217. A nucleic acid encoding the polypeptide of claim 207.
218. A nucleic acid encoding the polypeptide of claim 208.
219. A nucleic acid encoding the polypeptide of claim 209.

1/10

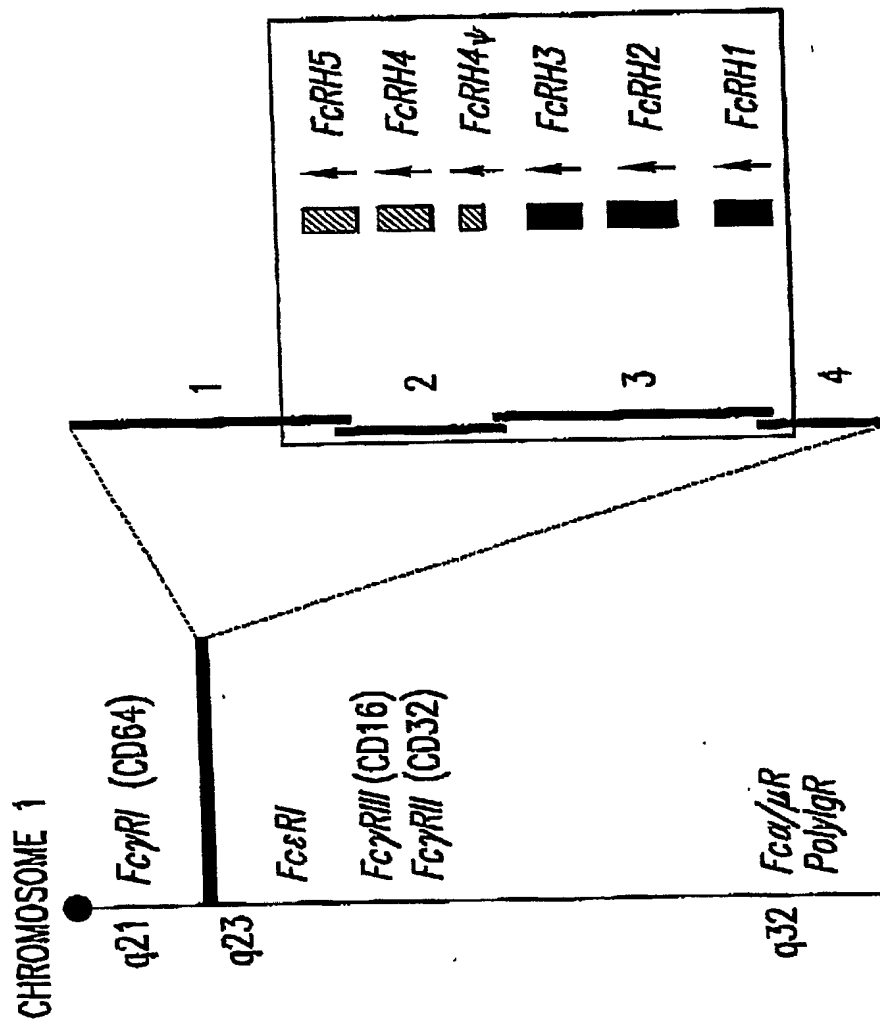


FIG.1

2/10

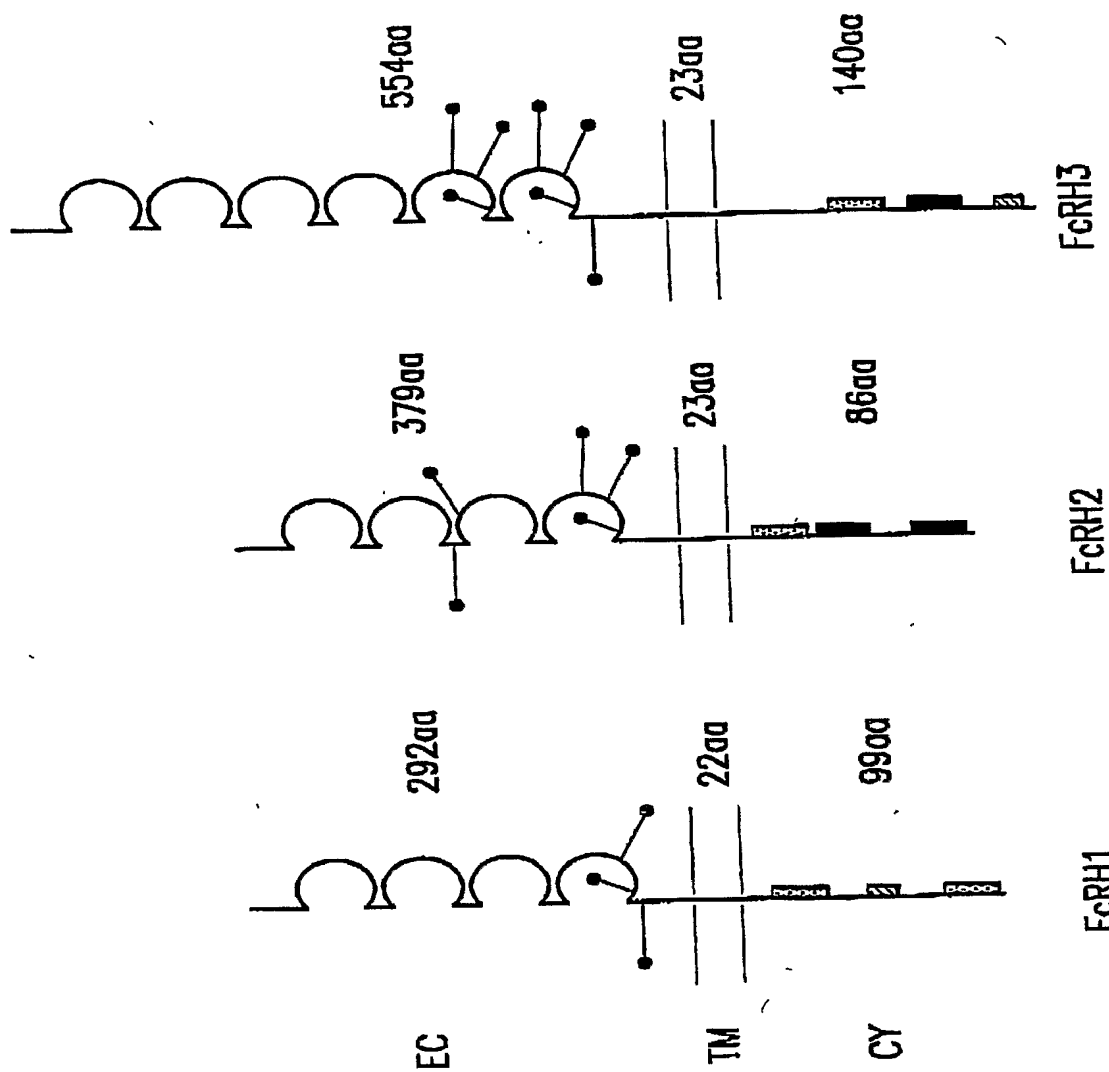


FIG. 2A

SP
 FCRH3 MLLWILLITL TPGREQS-- (17)
 FCRH2 S.V.F DAVT..ADS (19)
 FCRH1 ..PR.....C A.LC.P--- (16)

 EC1
 FCRH3 GWAPKAVULL NPPWSTAFKG EKVALTCSGI SHSLAQGDY WYHDEKLLKI KHDKIQITEP GNYCCKTRGS SLSDAVHVEF SP (82)
 FCRH2 -----
 FCRH1 -----

 EC2
 FCRH3 DWLLTLOALHP VFEQDNVILR CQCKONKNTH QKVYKDGKQ LPNSYNLERI TVNS-VSRON SKYHCTAYRK FYTILDEVTS KPLNIQVQ (87)
 FCRH2 --.T.V.PSSSIVLK ..EQ.WKIQ KWA.H..N.E .SVFKKFSDF LIQ.A.LS.S GN.F.STKGQ LFLW.K--- NIVK.K.. (84)
 FCRH1 -----

 EC3
 FCRH3 -ELFLHPVLR ASSSTPIEGS PMTLTCETQL SPQRPVQVQLQ FSLFRQSQTL GLGHSRSPRL QIPAWTETS GSYNCEVETV THSIKKRSLRS QIRVQ- (95)
 FCRH2 -...QR...T ..FQ...G ..VS.K...R.L.....CF..EN.V.S...S.E.S.V.S..TKA... ..R.R.Q..Q. ..H..R (95)
 FCRH1 A.....I .P.H.T.... V.....KNPF L-SS.A.F. CF...TRA. P...S.K. .A...K..TAQ..M ASKVL-R... ..N.H- (90)

 EC4
 FCRH3 RVPVSNWLE IRPTGGOLIE GENWVLICSV AQSGTIVTS WKEGRVRSI GRKTORSLLA ELHVLTVKES DAGRYVCAAD NVHSPILTSTW IRVTVR (96)
 FCRH2 -I.I...S...AP...VT. OKLILL... G.T.N... YR.AIGT.M .K.....S. .EIPA.... ..K...R... G.V..Q.KV VHIP... (95)
 FCRH1AD.S... TQ.P...VM. DRL..... M.T.OI..L Y.GAVGLN. QS.....T. YEIPS.R... ..EQ...V.E .GYG.SP.GL VSI... (96)

 EC5
 FCRH3 TPVSHPVLT F RAPRAHTVVG DILLEHGESL RGSPPILYRF YHEDVTLGNS SAPSGGASGF NLSLTAEHSG NYSCDAINGL GAQHSHEVSL RVT (93)
 FCRH2R...L S.G.QAA... ..A.Q.I...SRF.....E.N... ..R.EA.T. NF. (93)
 FCRH1R.I.MLQAA.E V.....A.W.I...SRF.....E.N... ..R.EA.T. NF. (93)

 EC6
 FCRH3 VPVSRPVLT RAPGAQAVVG DILLEHGESL RGSFPILYWF YHEDDTLGNI SAPSGGASGF NLSLTTEHSG NYSCDAINGL GAQHSKVVTL NVT (93)
 FCRH2 -----
 FCRH1 -----

FIG. 2B-1

[illegible]

4/10

FIG. 2B-2

5/10

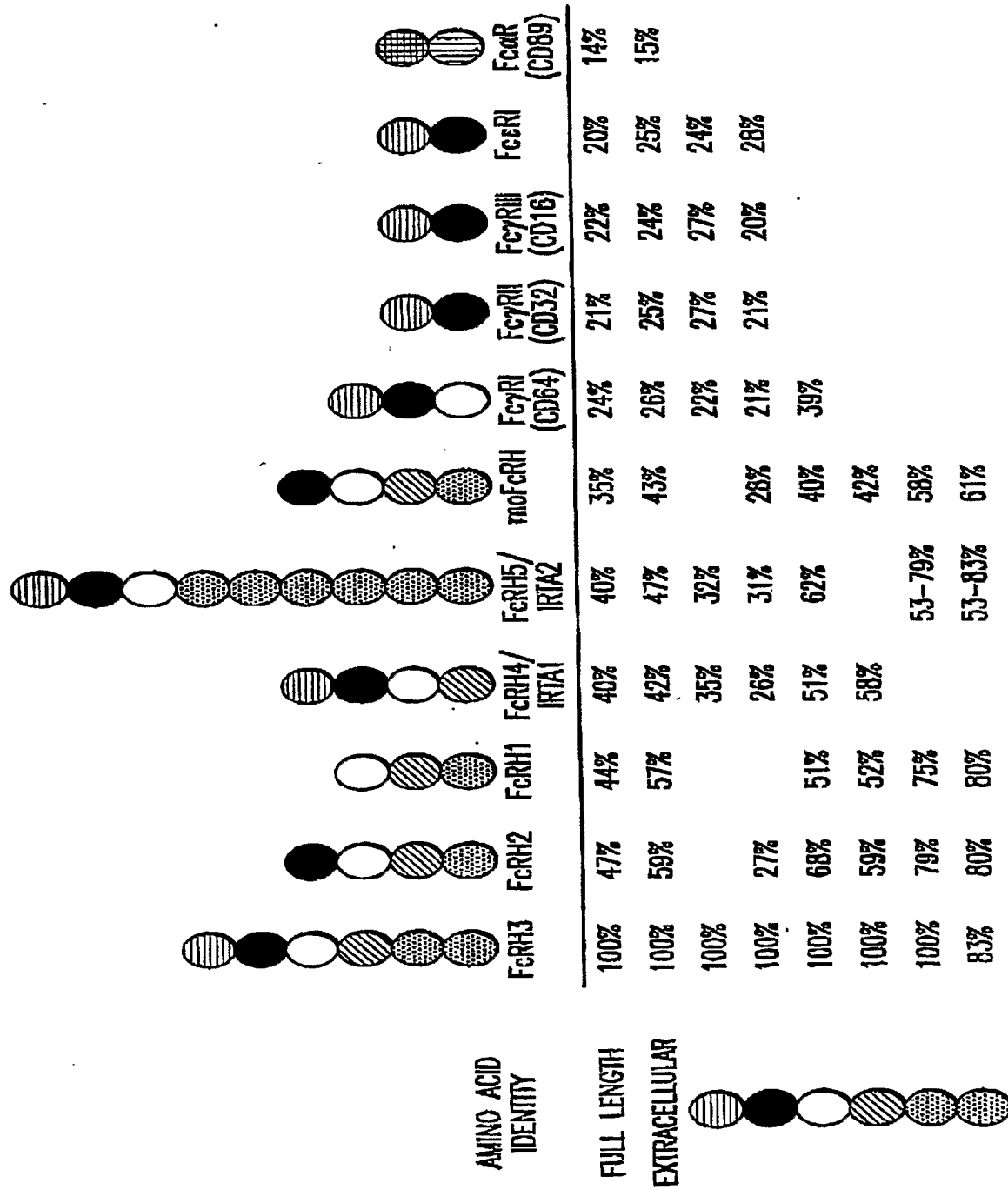


FIG.3

6/10

THE MOUSE *FcR* FAMILY IS SPLIT BETWEEN CHROMOSOMES 1 AND 3
IN REGIONS SYNTENIC WITH HUMAN CHROMOSOME 1q21-23
(THE *moFcRH* ARE LOCATED ON MOUSE Ch 3)

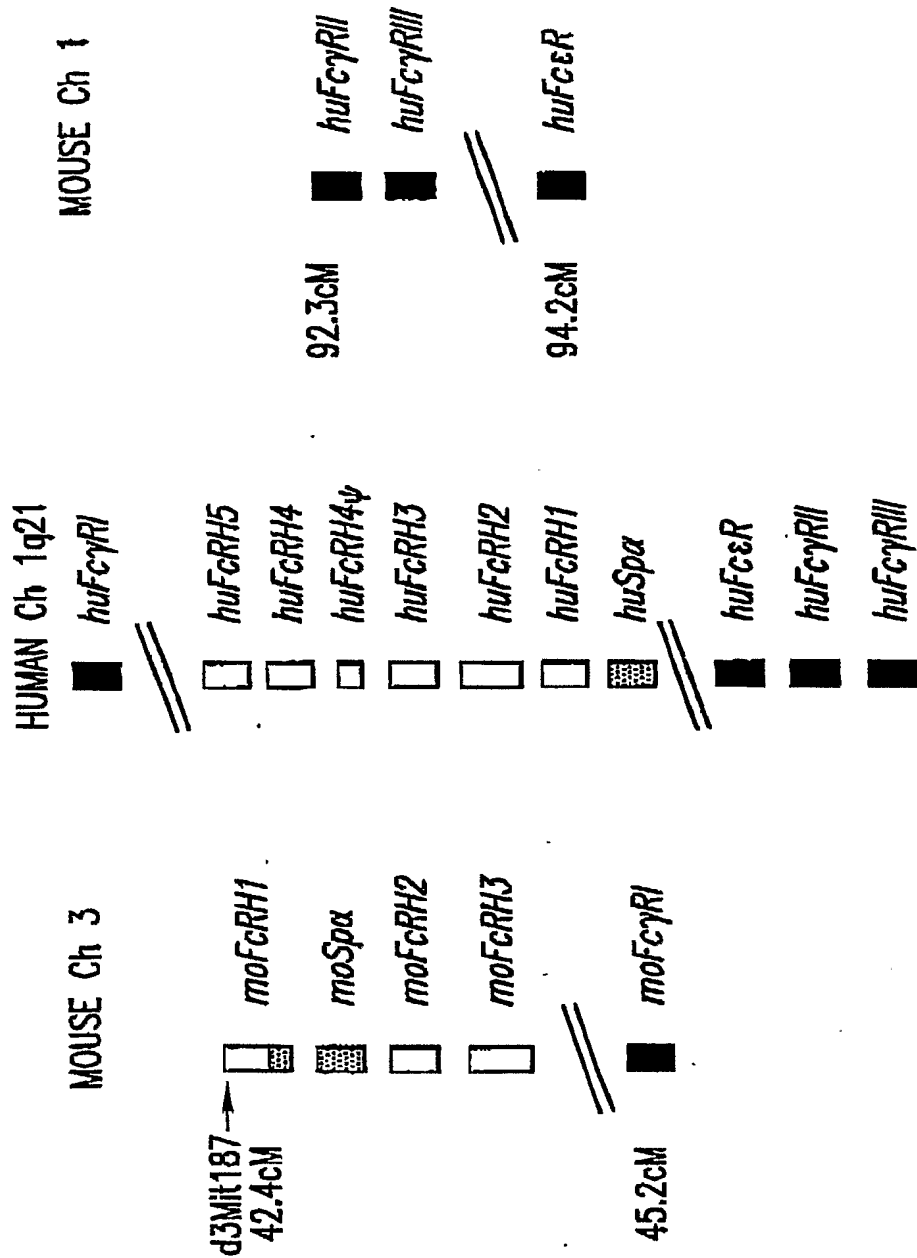


FIG.4

7/10

Comparison of Tyrosine Based Motifs in
FcRH Cytoplasmic Tails

| | | | |
|---------|----|---------------------------------------------------------------------------------------------------|----|
| huFcRH1 | 1 | -----KRKIGRRSARDPLRS-----LPSPLPQEFTYLN <u>SP</u> TP-GQLQPIYENNVN <u>VS</u> GDEVYSLAYYNQPEQE | 80 |
| huFcRH2 | | H-----KISGESSATNEPRG-----ASRPNPQEFTYSSPTPDMEELQPVYNNVGSVDVDVY <u>VSQ</u> WMSMQQPES | |
| huFcRH3 | | HYARARRKPGGLSATGTSSHPSECQEPSSRRSRIDPQEPHTSKPLAPME-LEPMYSNNVNP <u>GD</u> SNPIY <u>SQ</u> IWSIQHTKE | |
| huFcRH4 | | HCWRRRKSGVGFGLGDETRL-----PPAPGPGESSHSICPAQVE-LQSLYVDVHPKKGDL <u>Y</u> SEIQTITLQGE | |
| huFcRH5 | | -----SRKAGRKPAADPARS-----PSDSDSQEPTYHN-VPAAEELQPVYTNANPRGENVY <u>SE</u> IRIIQEKKK | |
| moFcRH2 | | -----KRKIGRQSE-DPVRS-----PPQTVLQGSTYPKSPDS-RQPEPLYENNVN <u>VS</u> GNIEYSLVYHTPQVLE | |
| moFcRH3 | | -----SRKAGGKPTSDSRN-----PSDSEPQEPTYYN-VPACIELOPVYSNE--PEENVY <u>Y</u> TEVRRTPRQK | |
| huFcRH1 | 81 | SVAAEITLGHMED---KVSIDIYSRLRKANITDV-----DYEDA-----M (99) | |
| huFcRH2 | | SAN--IRTLLENKDS---QVYYSYKK-----S (86) | |
| huFcRH3 | | NSANCPMMHQEHEEL----TVLYSELKTKHPDSDSAGEASSRGRAHEEDDEENYENVPRVLLASDH (140) | |
| huFcRH4 | | EEANTSRTILLEDKDV----SVVYSEVKTKQHPDNSAGKISSKD-----EES (107) | |
| huFcRH5 | | HAVASDPRHLRNKGS----PIIYSEVKVASTPVSGSLFLASS-----APHR (104) | |
| moFcRH2 | | PAAAQHVIRTHGVSESFQVSSGLYSKPR-INIAHM-----DYEDA-----M (100) | |
| moFcRH3 | | HAD-----QESSES-----PRSRCQM-----AEKK (79) | |

FIG.5

8/10

ANALYSIS OF SEQUENCE HOMOLOGY CONSERVATION
AMONG moFcRH AND huFcRH PROTEINS

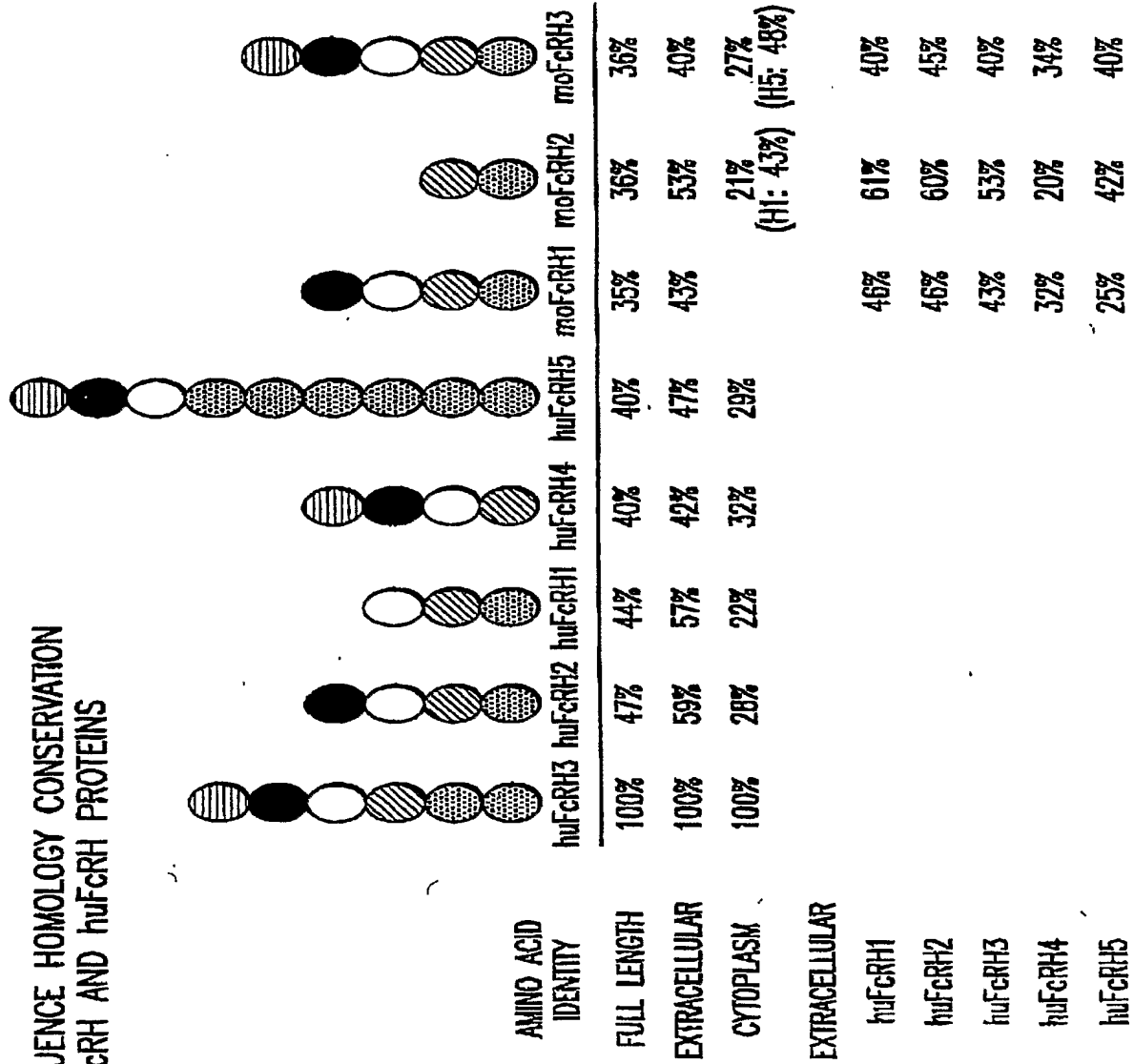


FIG.6

9/10

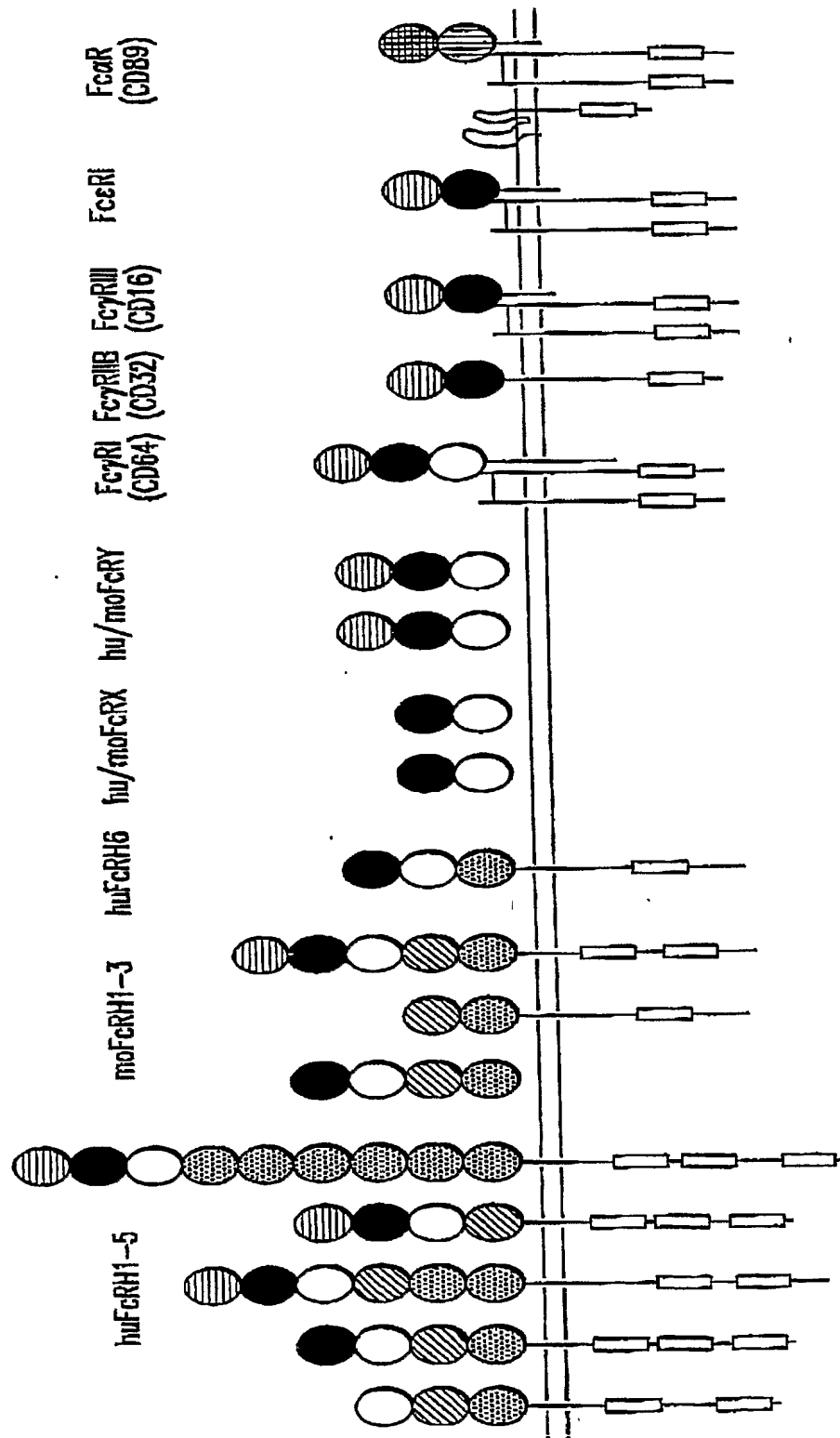


FIG. 7

10/10

CHARACTERISTICS OF moFcRH ISOFORMS

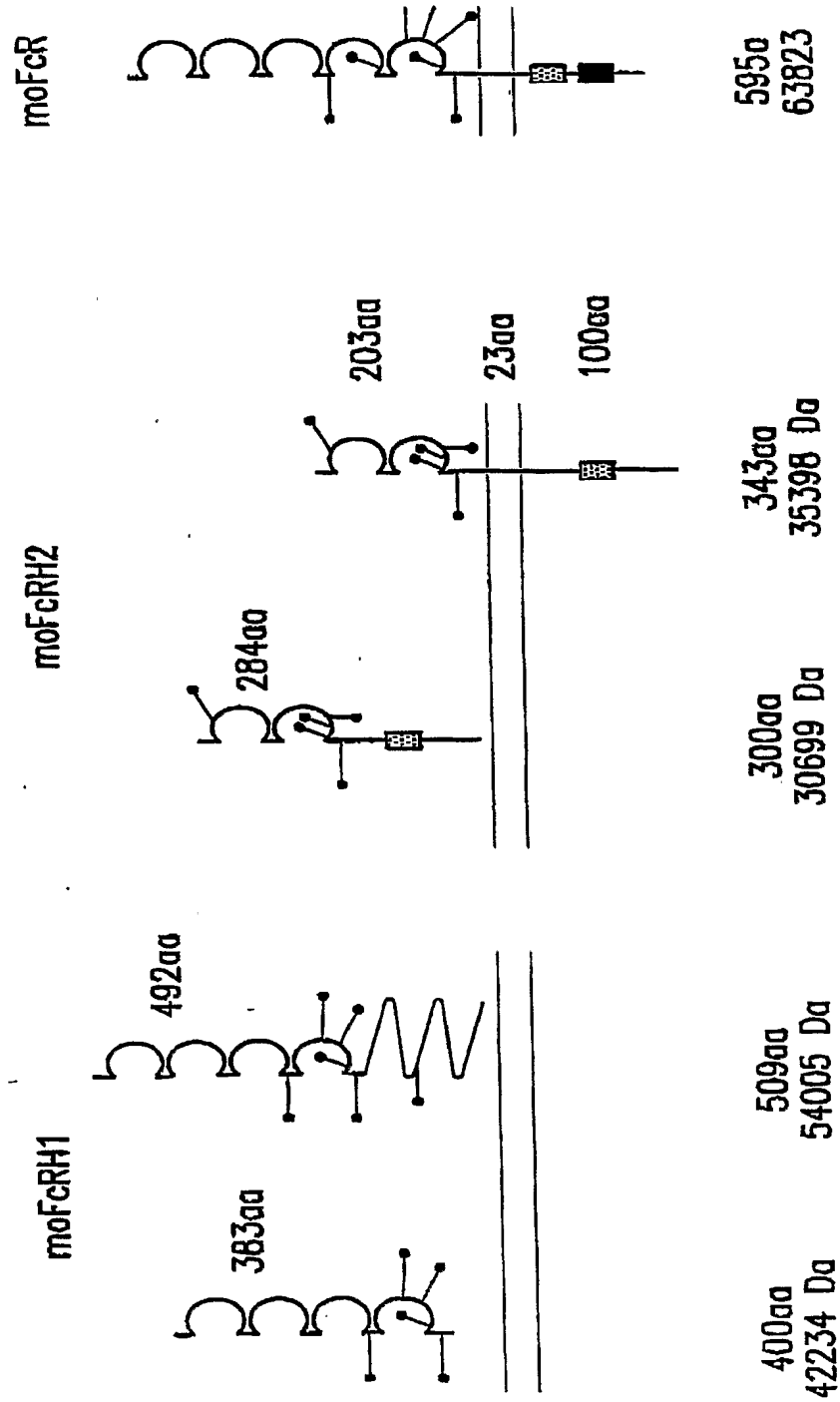


FIG.8

SEQUENCE LISTING

<110> The UAB Research Foundation
Davis, Randall S.
Cooper, Max D.

<120> MEMBERS OF THE FC RECEPTOR HOMOLOG GENE FAMILY (FCRH1-3, 6),
RELATED REAGENTS, AND USES THEREOF

<130> 21085.0037P1

<141> 2003-03-25

<150> US 60/367,667

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20 25 30
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35 40 45
Glu Val Tyr Ser Leu Ala Tyr Tyr Asn Gln Pro Glu Gln Glu Ser Val
50 55 60
Ala Ala Glu Thr Leu Gly Thr His Met Glu Asp Lys Val Ser Leu Asp
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Ile Tyr Ser Arg Leu Arg Lys Ala Asn Ile Thr Asp Val Asp Tyr Glu
85 90 95
Asp Ala Met

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20 25 30

Gln Phe Gln Phe Cys Phe Phe Arg Asp Thr Arg Ala Leu Gly Pro Gly
 35 40 45
 Trp Ser Ser Ser Pro Lys Leu Gln Ile Ala Ala Met Trp Lys Glu Asp
 50 55 60
 Thr Gly Ser Tyr Trp Cys Glu Ala Gln Thr Met Ala Ser Lys Val Leu
 65 70 75 80
 Arg Ser Arg Arg Ser Gln Ile Asn Val His Arg Val Pro Val Ala Asp
 85 90 95
 Val Ser Leu Glu Thr Gln Pro Pro Gly Gln Val Met Glu Gly Asp
 100 105 110
 Arg Leu Val Leu Ile Cys Ser Val Ala Met Gly Thr Gly Asp Ile Thr
 115 120 125
 Phe Leu Trp Tyr Lys Gly Ala Val Gly Leu Asn Leu Gln Ser Lys Thr
 130 135 140
 Gln Arg Ser Leu Thr Ala Glu Tyr Glu Ile Pro Ser Val Arg Glu Ser
 145 150 155 160
 Asp Ala Glu Gln Tyr Tyr Cys Val Ala Glu Asn Gly Tyr Gly Pro Ser
 165 170 175
 Pro Ser Gly Leu Val Ser Ile Thr Val Arg Ile Pro Val Ser Arg Pro
 180 185 190
 Ile Leu Met Leu Arg Ala Pro Arg Ala Gln Ala Ala Val Glu Asp Val
 195 200 205
 Leu Glu Leu His Cys Glu Ala Leu Arg Gly Ser Pro Pro Ile Leu Tyr
 210 215 220
 Trp Phe Tyr His Glu Asp Ile Thr Leu Gly Ser Arg Ser Ala Pro Ser
 225 230 235 240
 Gly Gly Gly Ala Ser Phe Asn Leu Ser Leu Thr Glu Glu His Ser Gly
 245 250 255
 Asn Tyr Ser Cys Glu Ala Asn Asn Gly Leu Gly Ala Gln Arg Ser Glu
 260 265 270
 Ala Val Thr Leu Asn Phe Thr Val Pro Thr Gly Ala Arg Ser Asn His
 275 280 285
 Leu Thr Ser Gly Val Ile Glu Gly Leu Leu Ser Thr Leu Gly Pro Ala
 290 295 300
 Thr Val Ala Leu Leu Phe Cys Tyr Gly Leu Lys Arg Lys Ile Gly Arg
 305 310 315 320
 Arg Ser Ala Arg Asp Pro Leu Arg Ser Leu Pro Ser Pro Leu Pro Gln
 325 330 335
 Glu Phe Thr Tyr Leu Asn Ser Pro Thr Pro Gly Gln Leu Gln Pro Ile
 340 345 350
 Tyr Glu Asn Val Asn Val Val Ser Gly Asp Glu Val Tyr Ser Leu Ala
 355 360 365
 Tyr Tyr Asn Gln Pro Glu Gln Glu Ser Val Ala Ala Glu Thr Leu Gly
 370 375 380
 Thr His Met Glu Asp Lys Val Ser Leu Asp Ile Tyr Ser Arg Leu Arg
 385 390 395 400
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 405 410

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 20 25 30
 Met Glu Glu Leu Gln Pro Val Tyr Val Asn Val Gly Ser Val Asp Val
 35 40 45
 Asp Val Val Tyr Ser Gln Val Trp Ser Met Gln Gln Pro Glu Ser Ser
 50 55 60
 Ala Asn Ile Arg Thr Leu Leu Glu Asn Lys Asp Ser Gln Val Ile Tyr
 65 70 75 80
 Ser Ser Val Lys Lys Ser
 85

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 20 25 30
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 35 40 45
 Leu Ile Gln Ser Ala Val Leu Ser Asp Ser Gly Asn Tyr Phe Cys Ser
 50 55 60
 Thr Lys Gly Gln Leu Phe Leu Trp Asp Lys Thr Ser Asn Ile Val Lys
 65 70 75 80
 Ile Lys Val Gln Glu Leu Phe Gln Arg Pro Val Leu Thr Ala Ser Ser
 85 90 95
 Phe Gln Pro Ile Glu Gly Gly Pro Val Ser Leu Lys Cys Glu Thr Arg
 100 105 110
 Leu Ser Pro Gln Arg Leu Asp Val Gln Leu Gln Phe Cys Phe Phe Arg
 115 120 125
 Glu Asn Gln Val Leu Gly Ser Gly Trp Ser Ser Ser Pro Glu Leu Gln
 130 135 140
 Ile Ser Ala Val Trp Ser Glu Asp Thr Gly Ser Tyr Trp Cys Lys Ala
 145 150 155 160
 Glu Thr Val Thr His Arg Ile Arg Lys Gln Ser Leu Gln Ser Gln Ile
 165 170 175
 His Val Gln Arg Ile Pro Ile Ser Asn Val Ser Leu Glu Ile Arg Ala
 180 185 190
 Pro Gly Gly Gln Val Thr Glu Gly Gln Lys Leu Ile Leu Leu Cys Ser
 195 200 205
 Val Ala Gly Gly Thr Gly Asn Val Thr Phe Ser Trp Tyr Arg Glu Ala
 210 215 220
 Thr Gly Thr Ser Met Gly Lys Lys Thr Gln Arg Ser Leu Ser Ala Glu
 225 230 235 240
 Leu Glu Ile Pro Ala Val Lys Glu Ser Asp Ala Gly Lys Tyr Tyr Cys
 245 250 255
 Arg Ala Asp Asn Gly His Val Pro Ile Gln Ser Lys Val Val Asn Ile
 260 265 270
 Pro Val Arg Ile Pro Val Ser Arg Pro Val Leu Thr Leu Arg Ser Pro
 275 280 285
 Gly Ala Gln Ala Ala Val Gly Asp Leu Leu Glu Leu His Cys Glu Ala
 290 295 300
 Leu Arg Gly Ser Pro Pro Ile Leu Tyr Gln Phe Tyr His Glu Asp Val

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305          310          315          320
Thr Leu Gly Asn Ser Ser Ala Pro Ser Gly Gly Gly Ala Ser Phe Asn
          325          330          335
Leu Ser Leu Thr Ala Glu His Ser Gly Asn Tyr Ser Cys Glu Ala Asn
          340          345          350
Asn Gly Leu Gly Ala Gln Cys Ser Glu Ala Val Pro Val Ser Ile Ser
          355          360          365
Gly Pro Asp Gly Tyr Arg Arg Asp Leu Met Thr Ala Gly Val Leu Trp
          370          375          380
Gly Leu Phe Gly Val Leu Gly Phe Thr Gly Val Ala Leu Leu Leu Tyr
385          390          395          400
Ala Leu Phe His Lys Ile Ser Gly Glu Ser Ser Ala Thr Asn Glu Pro
          405          410          415
Arg Gly Ala Ser Arg Pro Asn Pro Gln Glu Phe Thr Tyr Ser Ser Pro
          420          425          430
Thr Pro Asp Met Glu Glu Leu Gln Pro Val Tyr Val Asn Val Gly Ser
          435          440          445
Val Asp Val Asp Val Val Tyr Ser Gln Val Trp Ser Met Gln Gln Pro
          450          455          460
Glu Ser Ser Ala Asn Ile Arg Thr Leu Leu Glu Asn Lys Asp Ser Gln
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          20          25          30
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          35          40          45
Pro Met Glu Leu Glu Pro Met Tyr Ser Asn Val Asn Pro Gly Asp Ser
          50          55          60
Asn Pro Ile Tyr Ser Gln Ile Trp Ser Ile Gln His Thr Lys Glu Asn
65          70          75          80
Ser Ala Asn Cys Pro Met Met His Gln Glu His Glu Glu Leu Thr Val
          85          90          95
Leu Tyr Ser Glu Leu Lys Lys Thr His Pro Asp Asp Ser Ala Gly Glu
          100          105          110
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 35 40 45
 Lys Ile Lys His Asp Lys Ile Gln Ile Thr Glu Pro Gly Asn Tyr Gln
 50 55 60
 Cys Lys Thr Arg Gly Ser Ser Leu Ser Asp Ala Val His Val Glu Phe
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 Leu Glu Lys Ile Thr Val Asn Ser Val Ser Arg Asp Asn Ser Lys Tyr
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 Ser Lys Pro Leu Asn Ile Gln Val Gln Glu Leu Phe Leu His Pro Val
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 Thr Cys Glu Thr Gln Leu Ser Pro Gln Arg Pro Asp Val Gln Leu Gln
 195 200 205
 Phe Ser Leu Phe Arg Asp Ser Gln Thr Leu Gly Leu Gly Trp Ser Arg
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 Ser Pro Arg Leu Gln Ile Pro Ala Met Trp Thr Glu Asp Ser Gly Ser
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 Tyr Trp Cys Glu Val Glu Thr Val Thr His Ser Ile Lys Lys Arg Ser
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 325 330 335
 Gly Arg Tyr Tyr Cys Ala Ala Asp Asn Val His Ser Pro Ile Leu Ser
 340 345 350
 Thr Trp Ile Arg Val Thr Val Arg Ile Pro Val Ser His Pro Val Leu
 355 360 365
 Thr Phe Arg Ala Pro Arg Ala His Thr Val Val Gly Asp Leu Leu Glu
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 625 630 635 640
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 Asn Ser Ala Asn Cys Pro Met Met His Gln Glu His Glu Glu Leu Thr
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 Val Leu Tyr Ser Glu Leu Lys Lys Thr His Pro Asp Asp Ser Ala Gly
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tttagtccact gttaccaaatt tagaactaaa acaaagttac ataaaaagtt attgtgactc      1920
cacttaattt tagtgacgta tttttgtata tataggccaa cctataccac atccaaaatt      1980
atgtatctat tacagcccct agaagcttta taaatacagt gtgtcttctt ttattcac      2038

```

<210> 9
 <211> 261
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

```

<400> 9
cacaagatat caggagaaag ttctgccact aatgaaccca gaggggcttc caggccaaat      60
cctcaagagt tcacctattc aagcccaacc ccagacatgg aggagctgca gccagtgtat      120
gtcaatgtgg gctctgtaga tgtggatgtg gtttattctc aggtctggag catgcagca      180
ccagaaagct cagcaaacat caggacactt ctggagaaca aggactccca agtcatctac      240
tcttctgtga agaaatcata a

```

<210> 10
 <211> 2573
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

```

<400> 10
ggtgaccaag agtacatctc ttttcaaata gctggattag gtccatcatgc tgctgtgggtc      60
attgctgggtc atctttgatg cagtcaactga acaggcagat tcgctgaccc ttgtggcgcc      120

```

| | | | | | | |
|-------------|-------------|-------------|-------------|-------------|-------------|------|
| ctctttctgtc | ttcgaaggag | acagcatcgt | tctgaaatgc | cagggagaa | agaactggaa | 180 |
| aattcagaag | atggccttacc | ataaggataa | caaagagtta | tctgttttca | aaaaattctc | 240 |
| agatttctctt | atccaaagt | cagttttaag | tgacagtggg | aactatttct | gtagtaccaa | 300 |
| aggacaactc | tttctctggg | ataaaaacttc | aaatatagta | aagataaaaag | tccaagagct | 360 |
| ctttcaacgt | cctgtgctga | ctgccagctc | cttccagccc | atcgaagggg | gtccagtggag | 420 |
| cctgaaatgt | gagacccggc | tctctccaca | gaggttggat | gttcaactcc | agttctgtct | 480 |
| cttcagagaa | aaccagggtcc | tgggggtcagg | ctggagcagc | tctccggagc | tccagatttc | 540 |
| tgccgtgtgg | agtgaagaca | caggggtctta | ctgggtgcaag | gcagaaacgg | tgactcacag | 600 |
| gatcagaaaa | cagagcctcc | aatcccagat | tcacgtgcag | agaatcccca | tctctaattgt | 660 |
| aagcttggag | atccggggccc | cgggggggaca | ggtgactgaa | ggacaaaaac | tgatcctgct | 720 |
| ctgctcagtg | gctgggggta | caggaaatgt | cacattctcc | tggtacagag | aggccacagg | 780 |
| aaccagtatg | ggaaagaaaa | cccagcgttc | cctgtcagca | gagctggaga | tcccagctgt | 840 |
| gaaagagagt | gatgccggca | aatattactg | tagagctgac | aacggccatg | tgccctatcca | 900 |
| gagcaagggtg | gtgaatatcc | ctgtgagaat | tccagtgtct | cgccctgtcc | tcaccctcag | 960 |
| gtctcctggg | gcccaggctg | cagtggggga | cctgtctggag | cttcactgtg | aggccctgag | 1020 |
| aggctctccc | ccaatcttgt | accaatttta | tcatgaggat | gtcacccttg | ggaacagctc | 1080 |
| ggccccctct | ggaggagggg | cctccttcaa | cctctctttg | actgcagaa | attctggaaa | 1140 |
| ctactcctgt | gagggccaaca | acggcctggg | ggcccagtg | agtgaggcag | tgccagtctc | 1200 |
| catctcagga | cctgatggct | atagaagaga | cctcatgaca | gctggagttc | tctggggact | 1260 |
| gtttgggtgtc | cttgggtttca | ctggtgttgc | tttgcctgtg | tatgccttgt | tccacaagat | 1320 |
| atcaggagaa | agttctgcc | ctaataaacc | cagaggggct | tccaggccaa | atcctcaaga | 1380 |
| gttcacctat | tcaagcccaa | ccccagacat | ggaggagctg | cagccagtgt | atgtcaatgt | 1440 |
| gggctctgtg | gatgtggatg | tggtttattc | tcaggtctgg | agcatgcagc | agccagaaag | 1500 |
| ctcagcaaac | atcaggacac | ttctggagaa | caaggactcc | caagtcatct | actcttctgt | 1560 |
| gaagaaatca | taacacttgg | aggaatcaga | aggggaagatc | aacagcaagg | atggggcatc | 1620 |
| attaagactt | gctataaaa | cttatgaaaa | tgcttgaggc | ttatcacctg | ccacagccag | 1680 |
| aacgtgcctc | aggaggcacc | tcctgtcatt | tttgtcctga | tgatgtttct | tctccaatat | 1740 |
| cttctttttac | ctatcaatat | tcattgaact | gctgctacat | ccagacactg | tgcaaatata | 1800 |
| ttattttctgc | taccttctct | taagcaatca | gtgtgtaaaag | atttgaggga | agaatgaata | 1860 |
| agagatacaa | ggtctcacct | tcactactgt | tgaagtgtatg | agaacaggac | ttgatagtgg | 1920 |
| tgtattaact | tatttatgtg | ctgctggata | cagtttgcta | atattttgtt | gagaattttt | 1980 |
| gcaaatatgt | tcattgggaa | tattggcctg | aaattttctt | ttccactgtg | tctctgccag | 2040 |
| aatgttttgta | tcaggctgat | gctggccttca | tagaatgagt | taggcaggag | cccttccctcc | 2100 |
| ttgattttttt | ggcatagttt | cagcaggatt | ggtaccagtt | attctttctg | catcttgtag | 2160 |
| aattcagcta | tgaatccatc | tggtctaggg | cttttgtgtt | ggttggtaag | ttttttatta | 2220 |
| ctaattcaac | ttcagcgctt | gatattggct | taggaggggt | ttctgtctct | tcctgggttca | 2280 |
| atcttggggag | attgtgtgtt | tccaggaatt | tagccgtttc | ctccagattt | tcttctttat | 2340 |
| gtgcacgcac | ttgagtgtaa | acataactta | tatgcactgg | gaaacaaaaa | aatctgtgtg | 2400 |
| acttgcttta | ttgcagcatt | tgttttatatt | tggtagtctg | gaactgaacc | tgcaatatca | 2460 |
| ccaaagtatg | catatagttg | caaaaatgtg | atttttgaca | tagtaaatat | gagtatttgc | 2520 |
| aataaaactat | gatattactt | ttgtaagtat | atagaataaaa | atgtaataaa | tct | 2573 |

<210> 11

<211> 423

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 11

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| cattacgcca | gggcccgaag | gaaaccagga | ggactttctg | ccactggaac | atctagtcac | 60 |
| agtcctagcg | agtgtcagga | gccttctctg | tccaggcctt | ccaggataga | ccctcaagag | 120 |
| cccactcact | ctaaaccact | agccccaatg | gagctggagc | caatgtacag | caatgtaaat | 180 |
| cctggagata | gcaacccgat | ttattcccag | atctggagca | tccagcatac | aaaagaaaa | 240 |
| tcagctaatt | gtccaatgat | gcatcaagag | catgaggaac | ttacagtcct | ctattcagaa | 300 |
| ctgaagaaga | cacacccaga | cgactctgca | ggggaggcta | gcagcagagg | cagggcccat | 360 |
| gaagaagatg | atgaagaaaa | ctatgagaat | gtaccacgtg | tattactggc | ctcagaccac | 420 |
| tag | | | | | | 423 |

<210> 12
 <211> 2416
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

```

<400> 12
gtctcatctg agtagcagct tcctgccctc cttcttggag ataagtcggg cttttggtga      60
gacagacttt cccaaccctc tgcccgccg gtgcccattg ttctgtggct gctgctgctg      120
atcctgactc ctggaagaga acaatcaggg gtggcccca aagctgtact tctcctcaat      180
cctccatggt ccacagcctt caaaggagaa aaagtggtct tcatatgcag cagcatatca      240
cattccctag ccaggggaga cacatattgg tatcacgatg agaagttgtt gaaaaataaaa      300
catgacaaga tccaaattac agagcctgga aattaccaat gtaagaccgg aggatcctcc      360
ctcagtgatg ccgtgcatgt ggaattttca cccgactggc tgatcctgca ggctttacat      420
cctgtctttg aaggagacaa tgtcattctg agatgtcagg ggaaagacaa caaaaacact      480
catcaaaagg tttactacaa ggatggaaaa cagcttccta atagttataa tttagagaag      540
atcacagtga attcagtctc cagggataat agcaaataat attgtactgc ttataggaag      600
ttttacatac ttgacattga agtaacttca aaaccocctaa atatccaagt tcaagagctg      660
ttttacatac ctgtgctgag agccagctct tccacgcccc tagaggggag tcccatgacc      720
ctgacctgtg agaccagct ctctccacag aggccagatg tggagcaggt cccccagact ccagatccct      780
ttcagagata gccagaccct cggattgggc tggagcaggt cccccagact ccagatccct      840
gccatgttga ctgaagactc aggggtcttac tgggtgtgag tggagacagt gactcacagc      900
atcaaaaaaa ggagcctgag atctcagata cgtgtacaga gagtcocctgt gtctaattgtg      960
aatctagaga tccggccccc cggagggcag ctgattgaag gagaaaaatat ggtccttatt      1020
tgctcagtag cccaggggtt agggactgtc acattctcct ggcacaaaga aggaagagta      1080
agaagcctgg gtagaaagac ccagcgttcc ctgttggcag agctgcatgt tctcacctg      1140
aaggagagtg atgcaggag atactactgt gcagctgata acgttcacag ccccatcctc      1200
agcacgttga ttcgagtcac cgtgagaatt ccggtatctc accctgtcct caccttcagg      1260
gctcccaggg cccacactgt ggtgggggac ctgctggagc ttcactgtga gtccctgaga      1320
ggctctcccc cgatcctgta ccgattttat catgaggacg tcaccctggg gaacagctca      1380
gccccctctg gaggaggagc ctccctcaac ctctctctga ctgcagaaca ttctggaaac      1440
tactcctgtg atgcagacaa tggcctgggg gccagcaca gtcattggag gactctcagg      1500
gtcacagttc cgggtgtctg ccccgctcct accctcaggg ctcccggggc ccaggctgtg      1560
gtgggggacc tgctggagct tcaactgtgag tccctgagag gctccttccc gatcctgtac      1620
tggtttttat acgaggatga caccttgggg aacatctcgg cccactctgg aggaggggca      1680
tccttcaacc tctctctgac tacagaacat tctggaaact actcatgtga ggctgacaat      1740
ggcctggggg ccagcacag taaagtgggt acaactcaat ttacaggaac ttocaggaac      1800
agaacaggcc ttaccgctgc gggaatcacg gggctgggtc tcagcatcct cgtccttgct      1860
gctgctgctg ctctgctgca ttacgccagg gccgaagga aaccaggagg actttctgcc      1920
actggaacat ctagtccag tcttagcgag tgtcaggagc ctctctctgc caggccttcc      1980
aggatagacc ctcaagagcc cactcactct aaaccactag cccaatgga gctggagcca      2040
atgtacagca atgcaaatcc tggagatagc aaccgattt attcccagat ctggagcatc      2100
cagcatacaa aagaaaactc agctaattgt ccaatgatgc atcaagagca tgaggaaact      2160
acagtctctt attcagaact gaagaagaca caccagacg actctgcagg ggaggctagc      2220
agcagaggca gggcccatga agaagatgat gaagaaaact atgagaatgt accacgtgta      2280
ttactggcct cagaccacta gcccttacc cagagtggcc cacaggaaac agcctgcacc      2340
atTTTTTTTT ctgttctctc caaccacaca tcatccatct ctccagactc tgcctcctac      2400
gaggctgggc tgcagg                                     2416

```

<210> 13
 <211> 873
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

```

<400> 13
gagctgtttt tgatagccag cccctcccat cccacagagg ggagcccagt gaccctgacg      60
tgtaagatgc cctttctaca gagttcagat gccagttcc agttctgctt tttcagagac      120
acccgggcct tgggcccagg ctggagcagc tcccccaagc tccagatcgc tgccatgtgg      180
aaagaagaca cagggtcata ctgggtcgag gcacagacaa tggcgtccaa agtcttgagg      240
agcaggagat cccagataaa tgtgcacagg gtccctgtcg ctgatgtgag cttgggagact      300
cagcccccag gaggacaggt gatggaggga gacaggctgg tcctcatctg ctcagttgct      360
atggggcacag gagacatcac cttoctttgg taaaaagggg ctgtaggttt aaaccttcag      420
tcaaagacct agcgttcact gacagcagag tatgagattc cttcagttag ggagagtgat      480
gctgagcaat attactgtgt agctgaaaaat ggctatggtc ccagcccagc tgggctgggtg      540
agcatcactg tcagaatccc ggtgtctcgc ccaatcctca tgctcagggc tcccaggggc      600
caggctgcag tggaggtagt gctggagctt cactgtgagg ccctgagagg ctctcctcca      660
atcctgtact ggttttatca cgaggatata accctgggga gcaggctcggc cccctctgga      720
ggaggagcct ccttcaacct ttocctgact gaagaacatt ctggaaacta ctctgtgag      780
gccacaatg gcctgggggc ccagcgcagt gagggcgtga cactcaactt cacagtgcct      840
actggggcca gaagcaatca tcttacctca gga      873

```

```

<210> 14
<211> 1137
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:/note =
        synthetic construct

```

```

<400> 14
acccttgtgg cgccctcttc tgtcttcgaa ggagacagca tcgttctgaa atgccaggga      60
gaacagaact ggaaaattca gaagatggct taccataagg ataacaaaga gttatctgtt      120
ttcaaaaaat tctcagatctt ccttatccaa agtgcagttt taagtgcagc tggtaactat      180
ttctgtagta ccaaaggaca actctttctc tgggataaaa cttcaaatat agtaaagata      240
aaagtccaag agctctttca acgtcctgtg ctgactgcca gctccttcca gcccatcgaa      300
gggggtccag tgagcctgaa atgtgagacc cggctctctc cacagagggt ggatgttcaa      360
ctccagttct gcttcttcag agaaaaccag gtccctgggt caggctggag cagctctccg      420
gagctccaga tttctgcogt gtggagtga gacacagggt cttactgggt caaggcagaa      480
acggtgactc acaggatcag aaaacagagc ctccaatccc agattcacgt gcagagaatc      540
cccatctcta atgtaagctt ggagatccgg gccccgggg gacagggtgac tgaaggacaa      600
aaactgatcc tgctctgctc agtggctggg ggtacaggaa atgtcacatt ctccctgtac      660
agagaggcca caggaaccag tatgggaaag aaaaccagc gttccctgtc agcagagctg      720
gagatcccag ctgtgaaaga gagtgatgcc ggcaaataat actgtagagc tgacaacggc      780
catgtgccta tccagagcaa ggtggtgaat atccctgtga gaattccagt gtctcgccct      840
gtcctcacc tcaaggctctc tggggcccag gctgcagtgg gggacctgct ggagcttcac      900
tgtgaggccc tgagggtctc tcccccaatc ttgtaccaat tttatcatga ggatgtcacc      960
cttgggaaca gctcggcccc ctctggagga ggggcctcct tcaacctctc tttgactgca      1020
gaacattctg gaaactactc ctgtgaggcc aacaacggcc tggggggcca gtgcagttag      1080
gcagtgccag tctccatctc aggacctgat ggctatagaa gagacctcat gacagct      1137

```

```

<210> 15
<211> 1659
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:/note =
        synthetic construct

```

```

<400> 15
gtggcccca aagctgtact tctcctcaat cctccatggt ccacagcctt caaaggagaa      60
aaagtggctc tcatatgcag cagcataatca cattccctag ccaggggaga cacatatattg      120
tatcacgatg agaagttgtt gaaaataaaa catgacaaga tccaaattac agagcctgga      180
aattaccaat gtaagaccgc aggatcctcc ctcatgtatg ccgtgcatgt ggaattttca      240

```

```

cccgaactggc  tgatcctgca  ggctttacat  cctgtctttg  aaggagacaa  tgtcattctg  300
agatgtcagg  ggaaagacaa  caaaaacact  catcaaaagg  tttactacaa  ggatggaaaa  360
cagcttccta  atagttataa  tttagagaag  atcacagtga  attcagtctc  cagggataat  420
agcaaataatc  attgtactgc  ttataggaag  tttacatac  ttgacattga  agtaactta  480
aaaccctaa  atatccaagt  tcaagagctg  tttctacatc  ctgtgctgag  agccagctct  540
tccacgcca  tagaggggag  tcccatgacc  ctgacctgtg  agaccagct  ctctccacag  600
aggccagatg  tccagctgca  attctccctc  ttcagagata  gccagaccct  cggattgggc  660
tggagcagg  cccccagact  ccagatccct  gccatgtgga  ctgaagactc  agggctttac  720
tgggtgtgag  tggagacagt  gactcacagc  atcaaaaaaa  ggagcctgag  atctcagata  780
cgtgtacaga  gagtccctgt  gtctaattgt  aatctagaga  tccggccac  cggagggcag  840
ctgattgaag  gagaaaatat  ggtccttatt  tgctcagtag  cccaggggtc  agggactgtc  900
acattctcct  ggcacaaaag  aggaagagta  agaagcctgg  gtagaaagac  ccagcgttcc  960
ctgttggcag  agctgcatgt  tctcacctg  aaggagagtg  atgcaggagg  atactactgt  1020
gcagctgata  acgttcacag  ccccatcctc  agcacgtgga  ttcgagtcac  cgtgagaatt  1080
ccggtatctc  accctgtcct  caccttcagg  gctcccagg  cccacactgt  ggtgggggac  1140
ctgctggagc  ttcactgtga  gtccctgaga  ggctctcccc  cgatcctgta  ccgattttat  1200
catgaggacg  tcaccctggg  gaacagctca  gccccctctg  gaggaggagc  ctccctcaac  1260
ctctctctga  ctgcagaaca  ttctggaaac  tactcctgtg  atgcagacaa  tggcctgggg  1320
gccagcaca  gtcattggag  gactctcagg  gtcacagttc  cgggtgtctc  ccccgctcct  1380
accctcagg  ctcccgggg  ccaggctgtg  gtgggggacc  tgctggagct  tactgttgag  1440
tccctgagag  gctccttccc  gatcctgtac  tggttttatc  acgaggatga  caccttgggg  1500
aacatctcgg  cccactctgg  aggaggggca  tccttcaacc  tctctctgac  tacagaacat  1560
tctggaaact  actcatgtga  ggctgacaat  ggctggggg  cccagcacag  taaagtgggtg  1620
acactcaatg  ttacaggaac  ttccaggaac  agaacaggc  1659

```

<210> 16

<211> 423

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 16

```

cattacgcca  gggcccgaag  gaaaccagga  ggactttctg  ccaactggaac  atctagtcac  60
agtcctagcg  agtgtcagga  gccttctctg  tccaggcctt  ccaggataga  ccctcaagag  120
cccactcact  ctaaaccact  agccccaatg  gagctggagc  caatgtacag  caatgcaaat  180
cctggagata  gcaaccgat  ttattcccag  atctggagca  tccagcatac  aaaagaaaaa  240
tcagctaatt  gtccaatgat  gcatcaagag  catgaggaac  ttacagtcct  ctattcagaa  300
ctgaagaaga  cacaccaga  cgactctgca  ggggaggcta  gcagcagagg  cagggcccat  360
gaagaagatg  atgaagaaaa  ctatgagaat  gtaccacgtg  tattactggc  ctccagaccac  420
tag  423

```

<210> 17

<211> 2151

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 17

```

gtggcccaa  aagctgtact  tctcctcaat  cctccatggt  ccacagcctt  caaaggagaa  60
aaagtggctc  tcatatgcag  cagcatatca  cattccctag  cccagggaga  cacatattgg  120
tatcacgatg  agaagttgtt  gaaaaataaaa  catgacaaga  tccaaattac  agagcctgga  180
aattaccaat  gtaagaccgg  aggatcctcc  ctcagtgtatg  ccgtgcatgt  ggaattttca  240
cccgaactggc  tgatcctgca  ggctttacat  cctgtctttg  aaggagacaa  tgtcattctg  300
agatgtcagg  ggaaagacaa  caaaaacact  catcaaaagg  tttactacaa  ggatggaaaa  360
cagcttcta  atagttataa  tttagagaag  atcacagtga  attcagtctc  cagggataat  420

```

| | | | | | | |
|------------|-------------|------------|-------------|------------|-------------|------|
| agcaaatatc | attgtactgc | ttataggaag | ttttacatac | ttgacattga | agtaacttca | 480 |
| aaacccctaa | atatccaagt | tcaagagctg | tttctacatc | ctgtgctgag | agccagctct | 540 |
| tccacgcccc | tagaggggag | tcccatgacc | ctgacctgtg | agacccagct | ctctccacag | 600 |
| aggccagatg | tccagctgca | attctccctc | ttcagagata | gccagaccct | cggattgggc | 660 |
| tggagcagg | ccccagact | ccagatccct | gccatgtgga | ctgaagactc | aggggtcttac | 720 |
| tgggtgtgag | tggagacagt | gaotcacagc | atcaaaaaaa | ggagcctgag | atctcagata | 780 |
| cgtgtacaga | gagtccctgt | gtctaatgtg | aatctagaga | tccggcccac | cggagggcag | 840 |
| ctgattgaag | gagaaaatat | ggtocttatt | tgctcagtag | cccaggggtc | agggactgtc | 900 |
| acattctcct | ggcacaaaaga | aggaagagta | agaagcctgg | gtagaaagac | ccagcgttcc | 960 |
| ctgttggcag | agctgcatgt | tctcacctgt | aaggagagt | atgcagggag | atactactgt | 1020 |
| gcagctgata | acgtttcacag | ccccatcttc | agcacgtgga | ttcgagtcc | cgtgagaatt | 1080 |
| ccggtatctc | accctgtcct | caccttcagg | gctcccagg | cccacactgt | gggtgggggac | 1140 |
| ctgctggagc | ttcactgtga | gtccctgaga | ggctctcccc | cgatcctgta | ccgattttat | 1200 |
| catgaggacg | tcaccctggg | gaacagctca | gccccctctg | gaggaggagc | ctccttcaac | 1260 |
| ctctctctga | ctgcagaaca | ttctggaaac | tactcctgtg | atgcagacaa | tggcctgggg | 1320 |
| gcccagcaca | gtcatggagt | gagtctcagg | gtcacagtcc | tgctggagct | tcactgtgag | 1380 |
| accctcagg | ctcccggggc | ccaggctgtg | gtggggggacc | tgctggagct | tcactgtgag | 1440 |
| tccctgagag | gctccttccc | gatcctgtac | tggttttata | acgaggatga | caccttgggg | 1500 |
| aacatctcgg | cccactctgg | aggaggggca | tccttcaacc | tctctctgac | tacagaacat | 1560 |
| tctggaaact | actcatgtga | ggctgacaat | ggcctggggg | cccagcacag | taaagtgggtg | 1620 |
| acactcaatg | ttacaggaac | ttccaggaac | agaacaggcc | ttaccgctgc | gggaatcacg | 1680 |
| gggctgggtg | tcagcatcct | cgtccttgct | gctgctgctg | ctctgctgca | ttacgccagg | 1740 |
| gcccgaagga | aaccaggagg | actttctgct | actggaacat | ctagtccacg | tcctagcgag | 1800 |
| tgctcaggag | cttccctcgtc | caggccttcc | aggatagacc | ctcaagagcc | cactcactct | 1860 |
| aaaccactag | ccccaatgga | gctggagcca | atgtacagca | atgcaaatcc | tggagatagc | 1920 |
| aacccgattt | attcccagat | ctggagcatc | cagcatacaa | aagaaaactc | agctaattgt | 1980 |
| ccaatgatgc | atcaagagca | tgaggaaact | acagtcctct | attcagaact | gaagaagaca | 2040 |
| caccagacg | actctgcagg | ggaggctagc | agcagaggca | gggcccata | agaagatgat | 2100 |
| gaagaaaact | atgagaatgt | accacgtgta | ttactggcct | cagaccacta | g | 2151 |

<210> 18

<211> 315

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 18

| | | | | | | |
|------------|------------|-------------|------------|-------------|-------------|-----|
| agatcctgga | gaaaagctgg | gcccccttcca | tcccagatac | caccacacagc | tccaggtgga | 60 |
| gagcagtggc | cactatatgc | caacgtgcat | caccagaaag | ggaaagatga | aggtgttgct | 120 |
| tactctgtgg | tgcatagaac | ctcaaagagg | agtgaagcca | ggtctgctga | gttcaccgtg | 180 |
| gggagaaaag | acagttctat | catctgtgct | gaggtgagat | gcctgcagcc | cagtggaggtt | 240 |
| tcattccagg | aggtgaatat | gagaagcagg | actctccaag | aaccccttag | cgactgtgag | 300 |
| gaggttctct | gctag | | | | | 315 |

<210> 19

<211> 870

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 19

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| actgtctggc | tgtacctcca | agcctggcca | aaccctgtgt | ttgaaggaga | tgccctgact | 60 |
| ctgogatgtc | agggatggaa | gaatacacca | ctgtctcagg | tgaagttcta | cagagatgga | 120 |
| aaatttcctt | atttctctaa | ggaaaaccag | actctgtcca | tgggagcagc | aacagtgcag | 180 |
| agcogtggcc | agtacagctg | ctctgggcag | gtgatgtata | ttccacagac | attcacacaa | 240 |

```

acttcagaga ctgccatggt tcaagtccaa gagctgtttc cacctcctgt gctgagtgcc 300
atccccctctc ctgagccccg agagggtagc ctggtgaccc tgagatgtca gacaaagctg 360
caccocctga ggtagcctt gaggctcctt ttctccttcc acaaggacgg ccacaccttg 420
caggacaggg gccctcaccg agaactctgc atcccgggag ccaaggaggg agactctggg 480
ctttactggg gtgaggtggc ccctgagggg ggccagggtcc agaagcagag ccccagctg 540
gaggtcagag tgcaggctcc tgtatcccgt cctgtgtcca ctctgcacca cgggcctgct 600
gaccctgctg tgggggacat ggtgcagctc ctctgtgagg cacagagggg ctcccctccg 660
atcctgtatt ccttctacct tgatgagaag attgtgggga accactcagc tccctgtggg 720
ggaaccacct ccctcctctt cccagtgaag tcagaacagg atgctgggaa ctactcctgc 780
gaggtcgaga acagtgtctc cagagagagg agtgagccca agaagctgtc tctgaagggt 840
tctcaagtct tgttcaactcc cgccagcaac

```

<210> 20

<211> 1257

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 20

```

actgtctggc tgtacctcca agcctggcca aaccctgtgt ttgaaggaga tgccttgact 60
ctgcgatgtc agggatggaa gaatacacca ctgtctcagg tgaagttcta cagagatgga 120
aaattccttc atttctctaa ggaaaaccag actctgtcca tgggagcagc aacagtgcag 180
agccgtggcc agtacagctg ctctgggcag gtgatgtata ttccacagac attcacacaa 240
acttcagaga ctgccatggt tcaagtccaa gagctgtttc cacctcctgt gctgagtgcc 300
atccccctctc ctgagccccg agagggtagc ctggtgaccc tgagatgtca gacaaagctg 360
caccocctga ggtagcctt gaggctcctt ttctccttcc acaaggacgg ccacaccttg 420
caggacaggg gccctcaccg agaactctgc atcccgggag ccaaggaggg agactctggg 480
ctttactggg gtgaggtggc ccctgagggg ggccagggtcc agaagcagag ccccagctg 540
gaggtcagag tgcaggctcc tgtatcccgt cctgtgtcca ctctgcacca cgggcctgct 600
gaccctgctg tgggggacat ggtgcagctc ctctgtgagg cacagagggg ctcccctccg 660
atcctgtatt ccttctacct tgatgagaag attgtgggga accactcagc tccctgtggg 720
ggaaccacct ccctcctctt cccagtgaag tcagaacagg atgctgggaa ctactcctgc 780
gaggtcgaga acagtgtctc cagagagagg agtgagccca agaagctgtc tctgaagggt 840
tctcaagtct tgttcaactcc cgccagcaac tggctgggtc cttggcttcc tgcgagcctg 900
cttggcctga tgggttattgc tgctgcactt ctggtttatg tgagatcctg gagaaaagct 960
gggccccttc catcccagat accaccacac gctccagggtg gagagcagtg cccactatat 1020
gccaaactgc atcaccagaa agggaaagat gaaggtgttg tctactctgt ggtgcataga 1080
acctcaaaga ggagtgaagc caggctctgct gagttcaccg tgggggagaaa ggacagttct 1140
atcatctgtg cggaggtgag atgcoctgcag cccagtgagg tttcatccac ggaggtgaat 1200
atgagaagca ggactctcca agaaccctt agcgactgtg aggaggttct ctgctag 1257

```

<210> 21

<211> 292

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 21

```

Ala Glu Leu Phe Leu Ile Ala Ser Pro Ser His Pro Thr Glu Gly Ser
1           5           10           15
Pro Val Thr Leu Thr Cys Lys Met Pro Phe Leu Gln Ser Ser Asp Ala
20           25           30
Gln Phe Gln Phe Cys Phe Phe Arg Asp Thr Arg Ala Leu Gly Pro Gly
35           40           45

```


Trp Ser Ser Ser Pro Lys Leu Gln Ile Ala Ala Met Trp Lys Glu Asp
 50 55 60
 Thr Gly Ser Tyr Trp Cys Glu Ala Gln Thr Met Ala Ser Lys Val Leu
 65 70 75 80
 Arg Ser Arg Arg Ser Gln Ile Asn Val His Arg Val Pro Val Ala Asp
 85 90 95
 Val Ser Leu Glu Thr Gln Pro Pro Gly Gly Gln Val Met Glu Gly Asp
 100 105 110
 Arg Leu Val Leu Ile Cys Ser Val Ala Met Gly Thr Gly Asp Ile Thr
 115 120 125
 Phe Leu Trp Tyr Lys Gly Ala Val Gly Leu Asn Leu Gln Ser Lys Thr
 130 135 140
 Gln Arg Ser Leu Thr Ala Glu Tyr Glu Ile Pro Ser Val Arg Glu Ser
 145 150 155 160
 Asp Ala Glu Gln Tyr Tyr Cys Val Ala Glu Asn Gly Tyr Gly Pro Ser
 165 170 175
 Pro Ser Gly Leu Val Ser Ile Thr Val Arg Ile Pro Val Ser Arg Pro
 180 185 190
 Ile Leu Met Leu Arg Ala Pro Arg Ala Gln Ala Ala Val Glu Asp Val
 195 200 205
 Leu Glu Leu His Cys Glu Ala Leu Arg Gly Ser Pro Pro Ile Leu Tyr
 210 215 220
 Trp Phe Tyr His Glu Asp Ile Thr Leu Gly Ser Arg Ser Ala Pro Ser
 225 230 235 240
 Gly Gly Gly Ala Ser Phe Asn Leu Ser Leu Thr Glu Glu His Ser Gly
 245 250 255
 Asn Tyr Ser Cys Glu Ala Asn Asn Gly Leu Gly Ala Gln Arg Ser Glu
 260 265 270
 Ala Val Thr Leu Asn Phe Thr Val Pro Thr Gly Ala Arg Ser Asn His
 275 280 285
 Leu Thr Ser Gly
 290

<210> 22

<211> 380

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 22

Leu Thr Leu Val Ala Pro Ser Ser Val Phe Glu Gly Asp Ser Ile Val
 1 5 10 15
 Leu Lys Cys Gln Gly Glu Gln Asn Trp Lys Ile Gln Lys Met Ala Tyr
 20 25 30
 His Lys Asp Asn Lys Glu Leu Ser Val Phe Lys Lys Phe Ser Asp Phe
 35 40 45
 Leu Ile Gln Ser Ala Val Leu Ser Asp Ser Gly Asn Tyr Phe Cys Ser
 50 55 60
 Thr Lys Gly Gln Leu Phe Leu Trp Asp Lys Thr Ser Asn Ile Val Lys
 65 70 75 80
 Ile Lys Val Gln Glu Leu Phe Gln Arg Pro Val Leu Thr Ala Ser Ser
 85 90 95
 Phe Gln Pro Ile Glu Gly Gly Pro Val Ser Leu Lys Cys Glu Thr Arg
 100 105 110
 Leu Ser Pro Gln Arg Leu Asp Val Gln Leu Gln Phe Cys Phe Phe Arg
 115 120 125
 Glu Asn Gln Val Leu Gly Ser Gly Trp Ser Ser Ser Pro Glu Leu Gln
 130 135 140

```

Ile Ser Ala Val Trp Ser Glu Asp Thr Gly Ser Tyr Trp Cys Lys Ala
145          150          155          160
Glu Thr Val Thr His Arg Ile Arg Lys Gln Ser Leu Gln Ser Gln Ile
          165          170          175
His Val Gln Arg Ile Pro Ile Ser Asn Val Ser Leu Glu Ile Arg Ala
          180          185          190
Pro Gly Gly Gln Val Thr Glu Gly Gln Lys Leu Ile Leu Leu Cys Ser
          195          200          205
Val Ala Gly Gly Thr Gly Asn Val Thr Phe Ser Trp Tyr Arg Glu Ala
210          215          220
Thr Gly Thr Ser Met Gly Lys Lys Thr Gln Arg Ser Leu Ser Ala Glu
225          230          235          240
Leu Glu Ile Pro Ala Val Lys Glu Ser Asp Ala Gly Lys Tyr Tyr Cys
          245          250          255
Arg Ala Asp Asn Gly His Val Pro Ile Gln Ser Lys Val Val Asn Ile
          260          265          270
Pro Val Arg Ile Pro Val Ser Arg Pro Val Leu Thr Leu Arg Ser Pro
          275          280          285
Gly Ala Gln Ala Ala Val Gly Asp Leu Leu Glu Leu His Cys Glu Ala
290          295          300
Leu Arg Gly Ser Pro Pro Ile Leu Tyr Gln Phe Tyr His Glu Asp Val
305          310          315          320
Thr Leu Gly Asn Ser Ser Ala Pro Ser Gly Gly Gly Ala Ser Phe Asn
          325          330          335
Leu Ser Leu Thr Ala Glu His Ser Gly Asn Tyr Ser Cys Glu Ala Asn
          340          345          350
Asn Gly Leu Gly Ala Gln Cys Ser Glu Ala Val Pro Val Ser Ile Ser
          355          360          365
Gly Pro Asp Gly Tyr Arg Arg Asp Leu Met Thr Ala
          370          375          380

```

<210> 23

<211> 140

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 23

```

His Tyr Ala Arg Ala Arg Arg Lys Pro Gly Gly Leu Ser Ala Thr Gly
1          5          10          15
Thr Ser Ser His Ser Pro Ser Glu Cys Gln Glu Pro Ser Ser Ser Arg
          20          25          30
Pro Ser Arg Ile Asp Pro Gln Glu Pro Thr His Ser Lys Pro Leu Ala
          35          40          45
Pro Met Glu Leu Glu Pro Met Tyr Ser Asn Ala Asn Pro Gly Asp Ser
          50          55          60
Asn Pro Ile Tyr Ser Gln Ile Trp Ser Ile Gln His Thr Lys Glu Asn
          65          70          75          80
Ser Ala Asn Cys Pro Met Met His Gln Glu His Glu Glu Leu Thr Val
          85          90          95
Leu Tyr Ser Glu Leu Lys Lys Thr His Pro Asp Asp Ser Ala Gly Glu
          100          105          110
Ala Ser Ser Arg Gly Arg Ala His Glu Glu Asp Asp Glu Glu Asn Tyr
          115          120          125
Glu Asn Val Pro Arg Val Leu Ala Ser Asp His
          130          135          140

```

<210> 24

<211> 554

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 24

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Val | Ala | Pro | Lys | Ala | Val | Leu | Leu | Leu | Asn | Pro | Pro | Trp | Ser | Thr | 1 | 5 | 10 | 15 |
| Ala | Phe | Lys | Gly | Glu | Lys | Val | Ala | Leu | Ile | Cys | Ser | Ser | Ile | Ser | His | 20 | 25 | 30 | |
| Ser | Leu | Ala | Gln | Gly | Asp | Thr | Tyr | Trp | Tyr | His | Asp | Glu | Lys | Leu | Leu | 35 | 40 | 45 | |
| Lys | Ile | Lys | His | Asp | Lys | Ile | Gln | Ile | Thr | Glu | Pro | Gly | Asn | Tyr | Gln | 50 | 55 | 60 | |
| Cys | Lys | Thr | Arg | Gly | Ser | Ser | Leu | Ser | Asp | Ala | Val | His | Val | Glu | Phe | 65 | 70 | 75 | 80 |
| Ser | Pro | Asp | Trp | Leu | Ile | Leu | Gln | Ala | Leu | His | Pro | Val | Phe | Glu | Gly | 85 | 90 | 95 | |
| Asp | Asn | Val | Ile | Leu | Arg | Cys | Gln | Gly | Lys | Asp | Asn | Lys | Asn | Thr | His | 100 | 105 | 110 | |
| Gln | Lys | Val | Tyr | Tyr | Lys | Asp | Gly | Lys | Gln | Leu | Pro | Asn | Ser | Tyr | Asn | 115 | 120 | 125 | |
| Leu | Glu | Lys | Ile | Thr | Val | Asn | Ser | Val | Ser | Arg | Asp | Asn | Ser | Lys | Tyr | 130 | 135 | 140 | |
| His | Cys | Thr | Ala | Tyr | Arg | Lys | Phe | Tyr | Ile | Leu | Asp | Ile | Glu | Val | Thr | 145 | 150 | 155 | 160 |
| Ser | Lys | Pro | Leu | Asn | Ile | Gln | Val | Gln | Glu | Leu | Phe | Leu | His | Pro | Val | 165 | 170 | 175 | |
| Leu | Arg | Ala | Ser | Ser | Ser | Thr | Pro | Ile | Glu | Gly | Ser | Pro | Met | Thr | Leu | 180 | 185 | 190 | |
| Thr | Cys | Glu | Thr | Gln | Leu | Ser | Pro | Gln | Arg | Pro | Asp | Val | Gln | Leu | Gln | 195 | 200 | 205 | |
| Phe | Ser | Leu | Phe | Arg | Asp | Ser | Gln | Thr | Leu | Gly | Leu | Gly | Trp | Ser | Arg | 210 | 215 | 220 | |
| Ser | Pro | Arg | Leu | Gln | Ile | Pro | Ala | Met | Trp | Thr | Glu | Asp | Ser | Gly | Ser | 225 | 230 | 235 | 240 |
| Tyr | Trp | Cys | Glu | Val | Glu | Thr | Val | Thr | His | Ser | Ile | Lys | Lys | Arg | Ser | 245 | 250 | 255 | |
| Leu | Arg | Ser | Gln | Ile | Arg | Val | Gln | Arg | Val | Pro | Val | Ser | Asn | Val | Asn | 260 | 265 | 270 | |
| Leu | Glu | Ile | Arg | Pro | Thr | Gly | Gly | Gln | Leu | Ile | Glu | Gly | Glu | Asn | Met | 275 | 280 | 285 | |
| Val | Leu | Ile | Cys | Ser | Val | Ala | Gln | Gly | Ser | Gly | Thr | Val | Thr | Phe | Ser | 290 | 295 | 300 | |
| Trp | His | Lys | Glu | Gly | Arg | Val | Arg | Ser | Leu | Gly | Arg | Lys | Thr | Gln | Arg | 305 | 310 | 315 | 320 |
| Ser | Leu | Leu | Ala | Glu | Leu | His | Val | Leu | Thr | Val | Lys | Glu | Ser | Asp | Ala | 325 | 330 | 335 | |
| Gly | Arg | Tyr | Tyr | Cys | Ala | Ala | Asp | Asn | Val | His | Ser | Pro | Ile | Leu | Ser | 340 | 345 | 350 | |
| Thr | Trp | Ile | Arg | Val | Thr | Val | Arg | Ile | Pro | Val | Ser | His | Pro | Val | Leu | 355 | 360 | 365 | |
| Thr | Phe | Arg | Ala | Pro | Arg | Ala | His | Thr | Val | Val | Gly | Asp | Leu | Leu | Glu | 370 | 375 | 380 | |
| Leu | His | Cys | Glu | Ser | Leu | Arg | Gly | Ser | Pro | Pro | Ile | Leu | Tyr | Arg | Phe | 385 | 390 | 395 | 400 |
| Tyr | His | Glu | Asp | Val | Thr | Leu | Gly | Asn | Ser | Ser | Ala | Pro | Ser | Gly | Gly | 405 | 410 | 415 | |

Leu Arg Ser Gln Ile Arg Val Gln Arg Val Pro Val Ser Asn Val Asn
 260 265 270
 Leu Glu Ile Arg Pro Thr Gly Gly Gln Leu Ile Glu Gly Glu Asn Met
 275 280 285
 Val Leu Ile Cys Ser Val Ala Gln Gly Ser Gly Thr Val Thr Phe Ser
 290 295 300
 Trp His Lys Glu Gly Arg Val Arg Ser Leu Gly Arg Lys Thr Gln Arg
 305 310 315 320
 Ser Leu Leu Ala Glu Leu His Val Leu Thr Val Lys Glu Ser Asp Ala
 325 330 335
 Gly Arg Tyr Tyr Cys Ala Ala Asp Asn Val His Ser Pro Ile Leu Ser
 340 345 350
 Thr Trp Ile Arg Val Thr Val Arg Ile Pro Val Ser His Pro Val Leu
 355 360 365
 Thr Phe Arg Ala Pro Arg Ala His Thr Val Val Gly Asp Leu Leu Glu
 370 375 380
 Leu His Cys Glu Ser Leu Arg Gly Ser Pro Pro Ile Leu Tyr Arg Phe
 385 390 395 400
 Tyr His Glu Asp Val Thr Leu Gly Asn Ser Ser Ala Pro Ser Gly Gly
 405 410 415
 Gly Ala Ser Phe Asn Leu Ser Leu Thr Ala Glu His Ser Gly Asn Tyr
 420 425 430
 Ser Cys Asp Ala Asp Asn Gly Leu Gly Ala Gln His Ser His Gly Val
 435 440 445
 Ser Leu Arg Val Thr Val Pro Val Ser Arg Pro Val Leu Thr Leu Arg
 450 455 460
 Ala Pro Gly Ala Gln Ala Val Val Gly Asp Leu Leu Glu Leu His Cys
 465 470 475 480
 Glu Ser Leu Arg Gly Ser Phe Pro Ile Leu Tyr Trp Phe Tyr His Glu
 485 490 495
 Asp Asp Thr Leu Gly Asn Ile Ser Ala His Ser Gly Gly Gly Ala Ser
 500 505 510
 Phe Asn Leu Ser Leu Thr Thr Glu His Ser Gly Asn Tyr Ser Cys Glu
 515 520 525
 Ala Asp Asn Gly Leu Gly Ala Gln His Ser Lys Val Val Thr Leu Asn
 530 535 540
 Val Thr Gly Thr Ser Arg Asn Arg Thr Gly Leu Thr Ala Ala Gly Ile
 545 550 555 560
 Thr Gly Leu Val Leu Ser Ile Leu Val Leu Ala Ala Ala Ala Leu
 565 570 575
 Leu His Tyr Ala Arg Ala Arg Arg Lys Pro Gly Gly Leu Ser Ala Thr
 580 585 590
 Gly Thr Ser Ser His Ser Pro Ser Glu Cys Gln Glu Pro Ser Ser Ser
 595 600 605
 Arg Pro Ser Arg Ile Asp Pro Gln Glu Pro Thr His Ser Lys Pro Leu
 610 615 620
 Ala Pro Met Glu Leu Glu Pro Met Tyr Ser Asn Ala Asn Pro Gly Asp
 625 630 635 640
 Ser Asn Pro Ile Tyr Ser Gln Ile Trp Ser Ile Gln His Thr Lys Glu
 645 650 655
 Asn Ser Ala Asn Cys Pro Met Met His Gln Glu His Glu Leu Thr
 660 665 670
 Val Leu Tyr Ser Glu Leu Lys Lys Thr His Pro Asp Asp Ser Ala Gly
 675 680 685
 Glu Ala Ser Ser Arg Gly Arg Ala His Glu Glu Asp Asp Glu Glu Asn
 690 695 700
 Tyr Glu Asn Val Pro Arg Val Leu Leu Ala Ser Asp His
 705 710 715

<210> 26

<211> 104

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 26
 Arg Ser Trp Arg Lys Ala Gly Pro Leu Pro Ser Gln Ile Pro Pro Thr
 1 5 10 15
 Ala Pro Gly Gly Glu Gln Cys Pro Leu Tyr Ala Asn Val His His Gln
 20 25 30
 Lys Gly Lys Asp Glu Gly Val Val Tyr Ser Val Val His Arg Thr Ser
 35 40 45
 Lys Arg Ser Glu Ala Arg Ser Ala Glu Phe Thr Val Gly Arg Lys Asp
 50 55 60
 Ser Ser Ile Ile Cys Ala Glu Val Arg Cys Leu Gln Pro Ser Glu Val
 65 70 75 80
 Ser Ser Thr Glu Val Asn Met Arg Ser Arg Thr Leu Gln Glu Pro Leu
 85 90 95
 Ser Asp Cys Glu Glu Val Leu Cys
 100

<210> 27
 <211> 291
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 27
 Lys Thr Val Trp Leu Tyr Leu Gln Ala Trp Pro Asn Pro Val Phe Glu
 1 5 10 15
 Gly Asp Ala Leu Thr Leu Arg Cys Gln Gly Trp Lys Asn Thr Pro Leu
 20 25 30
 Ser Gln Val Lys Phe Tyr Arg Asp Gly Lys Phe Leu His Phe Ser Lys
 35 40 45
 Glu Asn Gln Thr Leu Ser Met Gly Ala Ala Thr Val Gln Ser Arg Gly
 50 55 60
 Gln Tyr Ser Cys Ser Gly Gln Val Met Tyr Ile Pro Gln Thr Phe Thr
 65 70 75 80
 Gln Thr Ser Glu Thr Ala Met Val Gln Val Gln Glu Leu Phe Pro Pro
 85 90 95
 Pro Val Leu Ser Ala Ile Pro Ser Pro Glu Pro Arg Glu Gly Ser Leu
 100 105 110
 Val Thr Leu Arg Cys Gln Thr Lys Leu His Pro Leu Arg Ser Ala Leu
 115 120 125
 Arg Leu Leu Phe Ser Phe His Lys Asp Gly His Thr Leu Gln Asp Arg
 130 135 140
 Gly Pro His Pro Glu Leu Cys Ile Pro Gly Ala Lys Glu Gly Asp Ser
 145 150 155 160
 Gly Leu Tyr Trp Cys Glu Val Ala Pro Glu Gly Gly Gln Val Gln Lys
 165 170 175
 Gln Ser Pro Gln Leu Glu Val Arg Val Gln Ala Pro Val Ser Arg Pro
 180 185 190
 Val Leu Thr Leu His His Gly Pro Ala Asp Pro Ala Val Gly Asp Met
 195 200 205
 Val Gln Leu Leu Cys Glu Ala Gln Arg Gly Ser Pro Pro Ile Leu Tyr
 210 215 220

Ser Phe Tyr Leu Asp Glu Lys Ile Val Gly Asn His Ser Ala Pro Cys
 225 230 235 240
 Gly Gly Thr Thr Ser Leu Leu Phe Pro Val Lys Ser Glu Gln Asp Ala
 245 250 255
 Gly Asn Tyr Ser Cys Glu Ala Glu Asn Ser Val Ser Arg Glu Arg Ser
 260 265 270
 Glu Pro Lys Lys Leu Ser Leu Lys Gly Ser Gln Val Leu Phe Thr Pro
 275 280 285
 Ala Ser Asn
 290

<210> 28
 <211> 419
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 28
 Lys Thr Val Trp Leu Tyr Leu Gln Ala Trp Pro Asn Pro Val Phe Glu
 1 5 10 15
 Gly Asp Ala Leu Thr Leu Arg Cys Gln Gly Trp Lys Asn Thr Pro Leu
 20 25 30
 Ser Gln Val Lys Phe Tyr Arg Asp Gly Lys Phe Leu His Phe Ser Lys
 35 40 45
 Glu Asn Gln Thr Leu Ser Met Gly Ala Ala Thr Val Gln Ser Arg Gly
 50 55 60
 Gln Tyr Ser Cys Ser Gly Gln Val Met Tyr Ile Pro Gln Thr Phe Thr
 65 70 75 80
 Gln Thr Ser Glu Thr Ala Met Val Gln Val Gln Glu Leu Phe Pro Pro
 85 90 95
 Pro Val Leu Ser Ala Ile Pro Ser Pro Glu Pro Arg Glu Gly Ser Leu
 100 105 110
 Val Thr Leu Arg Cys Gln Thr Lys Leu His Pro Leu Arg Ser Ala Leu
 115 120 125
 Arg Leu Leu Phe Ser Phe His Lys Asp Gly His Thr Leu Gln Asp Arg
 130 135 140
 Gly Pro His Pro Glu Leu Cys Ile Pro Gly Ala Lys Glu Gly Asp Ser
 145 150 155 160
 Gly Leu Tyr Trp Cys Glu Val Ala Pro Glu Gly Gly Gln Val Gln Lys
 165 170 175
 Gln Ser Pro Gln Leu Glu Val Arg Val Gln Ala Pro Val Ser Arg Pro
 180 185 190
 Val Leu Thr Leu His His Gly Pro Ala Asp Pro Ala Val Gly Asp Met
 195 200 205
 Val Gln Leu Leu Cys Glu Ala Gln Arg Gly Ser Pro Pro Ile Leu Tyr
 210 215 220
 Ser Phe Tyr Leu Asp Glu Lys Ile Val Gly Asn His Ser Ala Pro Cys
 225 230 235 240
 Gly Gly Thr Thr Ser Leu Leu Phe Pro Val Lys Ser Glu Gln Asp Ala
 245 250 255
 Gly Asn Tyr Ser Cys Glu Ala Glu Asn Ser Val Ser Arg Glu Arg Ser
 260 265 270
 Glu Pro Lys Lys Leu Ser Leu Lys Gly Ser Gln Val Leu Phe Thr Pro
 275 280 285
 Ala Ser Asn Trp Leu Val Pro Trp Leu Pro Ala Ser Leu Leu Gly Leu
 290 295 300
 Met Val Ile Ala Ala Ala Leu Leu Val Tyr Val Arg Ser Trp Arg Lys
 305 310 315 320

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 32

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Leu | Trp | Thr | Ala | Val | Leu | Leu | Phe | Val | Pro | Cys | Val | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |

<210> 33

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 33

atgctgccga ggctgttgct gttgatctgt gctccactct gtgaacctgc c 51

<210> 34

<211> 1236

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 34

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| gagctgtttt | tgatagccag | cccctcccat | cccacagagg | ggagcccagt | gaccctgacg | 60 |
| tgtaagatgc | cctttctaca | gagttcagat | gcccagttcc | agttctgctt | tttcagagac | 120 |
| acccgggcct | tgggcccagg | ctggagcagc | tccccaaagc | tccagatcgc | tgccatgtgg | 180 |
| aaagaagaca | cagggtcata | ctggtgagag | gcacagacaa | tggcgtccaa | agtcttgagg | 240 |
| agcaggagat | cccagataaa | tgtgcacagg | gtccctgtcg | ctgatgtgag | cttgaggact | 300 |
| cagccccag | gaggacaggt | gatggaggga | gacaggctgg | tcctcatctg | ctcagttgct | 360 |
| atgggcacag | gagacatcac | cttccttttg | tacaaagggg | ctgtagggtt | aaaccttcag | 420 |
| tcaaagaccc | agcgttcact | gacagcagag | tatgagattc | cttcagttag | ggagagtgat | 480 |
| gctgagcaat | attactgtgt | agctgaaaat | ggctatggtc | ccagccccag | tgggctgggtg | 540 |
| agcatcactg | tcagaatccc | ggtgtctcgc | ccaatcctca | tgctcagggc | tcccagggcc | 600 |
| caggctgcag | tggaggatgt | gctggagctt | cactgtgagg | ccctgagagg | ctctcctcca | 660 |
| atcctgtact | ggttttatca | cgaggatata | accctgggga | gcaggtcggc | cccctctgga | 720 |
| ggaggagcct | ccttcaacct | ttccctgact | gaagaacatt | ctggaaacta | ctcctgtgag | 780 |
| gccaacaatg | gcctgggggc | ccagcgcagt | gaggcgggtg | cactcaactt | cacagtgcct | 840 |
| actggggcca | gaagcaatca | tcttacctca | ggagtcattg | aggggctgct | cagcaccctt | 900 |
| ggtccagcca | cgtggcctt | attattttgc | tacggcctca | aaagaaaaat | aggaagacgt | 960 |
| tcagccaggg | atccactcag | gagccttccc | agcctcttac | cccaagagtt | cacctacctc | 1020 |
| aactcaccta | ccccagggca | gctacagcct | atatatgaaa | atgtgaatgt | tgtaagtggg | 1080 |
| gatgaggttt | attcactggc | gtactataac | cagccggagc | aggaatcagt | agcagcagaa | 1140 |
| accctgggga | cacatatgga | ggacaagggt | tccttagaca | tctattccag | gctgaggaaa | 1200 |
| gcaaacatta | cagatgtgga | ctatgaagat | gctatg | | | 1236 |

<210> 35

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =

synthetic construct

<400> 35
atgctgctgt ggtcattgct ggtcatcttt gatgcagtca ctgaacaggc agattcgctg 60

<210> 36
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 36
acccttgtgg cgccctcttc tgtcttcgaa ggagacagca tcgttctgaa atgccaggga 60
gaacagaact ggaaaattca gaagatggct taccataagg ataacaaaga gttatctgtt 120
ttcaaaaaat tctcagatctt ctttatccaa agtgcagttt taagtgcagag tggtaactat 180
ttctgtagta ccaaaggaca actctttctc tgggataaaa cttcaaatat agtaaagata 240
aaagtccaag agctctttca acgtcctgtg ctgactgcca gctccttcca gcccatcgaa 300
gggggtccag tgagcctgaa atgtgagacc cggctctctc cacagagggt ggatgttcaa 360
ctccagttct gcttcttcag agaaaaccag gtcctggggt caggctggag cagctctccg 420
gagctccaga tttctgccgt gtggagtga gacacagggt cttactgggt caaggcagaa 480
accggtgact acaggatcag aaaacagagc ctccaatccc agattcacgt gcagagaatc 540
cccatctcta atgtaagctt ggagatccgg gccccgggg gacagggtgac tgaaggacaa 600
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atctactctt ctgtgaagaa atca 1464

<210> 37
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 37
atgcttctgt ggctgctgct gctgatcctg actcctggaa gagaacaatc aggg 54

<210> 38
<211> 2148
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

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<400> 38
gtggccccc aaagctgtact tctcctcaat cctccatggt ccacagcctt caaaggagaa      60
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tatcacgatg agaagttggt gaaaataaaa catgacaaga tccaaattac agagcctgga      180
aattaccaat gtaagaccog aggatcctcc ctgagtgatg ccgtgcatgt ggaattttca      240
cccgactggc tgatcctgca ggctttacat cctgtctttg aaggagacaa tgtcattctg      300
agatgtcagg ggaaagacaa caaaaacact catcaaaagg tttactacaa ggatggaaaa      360
cagcttccta atagttataa tttagagaag atcacagtga attcagtctc cagggataat      420
agcaaatatc attgtactgc ttataggaag ttttacatc ctgtgctgag agtaacttca      480
aaaccctaa atataccaagt tcaagagctg tttctacatc ctgtgctgag agccagctct      540
tccacgcca tagaggggag tcccatgacc ctgacctgtg agaccagct ctctccacag      600
aggccagatg tccagctgca attctccctc ttcagagata gccagaccct cggattgggc      660
tgagcagagt cccccagact ccagatccct gccatgtgga ctgaagactc aggggtttac      720
tggtgtgagg tggagacagt gactcacagc atcaaaaaaa ggagcctgag atctcagata      780
cgtgtacaga ggtccctgtg gtctaattgt aatctagaga tccggcccac cggaggcag      840
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acattctcct ggcacaaaaga aggaagagta agaagcctgg gtagaaagac ccagcgttcc      960
ctgttggcag agctgcatgt tctcacctg aaggagagt atgcaggag atactactgt      1020
gcagctgata acgttcacag cccatccctc agcacgtgga ttcgagtcac cgtgagaatt      1080
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ccaatgatgc atcaagagca tgaggaaact acagtcctct attcagaact gaagaagaca      2040
caccagacg actctgcagg ggaggctagc agcagaggca gggcccatga agaagatgat      2100
gaagaaaact atgagaatgt accacgtgta ttactggcct cagaccac      2148

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<210> 39
<211> 48
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:/note =
        synthetic construct

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<400> 39
atgctgctct ggacggctgt gctgctcttt gttccctgtg ttgggaaa      48

```

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<210> 40
<211> 2003
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:/note =
        synthetic construct

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<400> 40

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agggtctggtt gctctctgcc ggcttcgccc tgacctgttt ctgacctgtg ttccctccgc      60
tgtgccagaa caggcccccatt gctgctctgg acggctgtgc tgctctttgt tccctgtgtt      120
gggaaaactg tctggctgta cctccaagcc tggccaaacc ctgtgtttga aggagatgcc      180
ctgactctgc gatgtcaggg atggaagaat acaccactgt ctgaggtgaa gttctacaga      240
gatggaaaaa tccttcattt ctctaaggaa aaccagactc tgtccatggg agcagcaaca      300
gtgcagagcc gtggccagta cagctgctct gggcaggtga tgtatattcc acagacattc      360
acacaaactt cagagactgc catggttcaa gtccaagagc tgtttccacc tcctgtgctg      420
agtgccatcc cctctcctga gcccgcagag ggtagcctgg tgacctgag atgtcagaca      480
aagctgcacc ccctgagggtc agccttgagg ctccctttct cctccacaa ggacggccac      540
accttgcagg acagggggccc tcacccagaa ctctgcatcc cgggagccaa ggagggagac      600
tctgggcttt actgggtgtga ggtggccctt gaggggtggc aggtccagaa gcagagcccc      660
cagctggagg tcagagtgcg ggctcctgta tcccgctctg tgctcactct gcaccacggg      720
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cctccgatcc tgtattcctt ctacottgat gagaagattg tggggaacca ctgagctccc      840
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cccaatatat atatatatat gaaatagtca tgtgcgcgat aacaacattt cagtcagtga      1740
tagactgcat acacaacagt ggtcccataa gactgtaatg gagtttaaaa attcctactg      1800
octagtgata tcatagttgc cttaacatca taacacaaca catttctcac gcgtttgtgg      1860
tgatgctggt acaaacaagc tacagcgccg ctagtcatat acaaatatag cacatacaat      1920
tatgtacagt acactatact tgataatgat aataaacaac tatgttactg gtctaaaaaa      1980
aaaaaaaaaa aaaaaaaaaa aaa                                     2003

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<210> 41

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 41

tgagtctcag ggtcacagtt ccg

23

<210> 42

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 42

gctcttgaac ttggatatatt aggggt

26

<210> 43

<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 43 25
ccagtgtatg tcaatgtggg ctctg

<210> 44
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 44 27
cgttgaaaga gctcttggac ttttato

<210> 45
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 45 27
gcctcaaaag aaaaatagga agacgtt

<210> 46
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 46 23
aagctcacat cagcgacagg gac

<210> 47
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 47 22
tcttgagat aagtcgggct tt

<210> 48
<211> 25
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 48
atcctgcagc ccagcctogt aggag

25

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 49
ggtcctcatg ctgctgtggt catt

24

<210> 50
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 50
gctgttgatc ttcccttctg attc

24

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 51
atgctgccga ggctgttgct gttg

24

<210> 52
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 52
catagcatct tcatagtcca catc

24

<210> 53
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 53
ctcaacttca cagtgcctac tggg 24

<210> 54
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 54
tcctgcagag tcactaacct tgag 24

<210> 55
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 55
ccagtgtatg tcaatgtggg ctctg 25

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 56
cattcttccc tcaaattcttt acac 24

<210> 57
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 57
cagcacgtgg attcgagtca c 21

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 58
cagatctggg aataaatcgg gttg 24

<210> 59
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 59
tcttcagaga tggcgaggtc a 21

<210> 60
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 60
ttttggggtg tacatcaaca tacaag 26

<210> 61
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 61
tgttgccctg tttcttccaa taca 24

<210> 62
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 62
cagagttggc cgacctacgc 20

<210> 63
<211> 32
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<221> VARIANT

<222> 5, 15, 17, 22, 28

<223> X can be any amino acid

<400> 63

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Glu | Pro | Ile | Xaa | Leu | Arg | Cys | His | Ser | Trp | Lys | Asp | Lys | Xaa | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Xaa | Lys | Val | Thr | Tyr | Xaa | Gln | Asn | Gly | Lys | Ala | Xaa | Lys | Phe | Phe | His |
| | | | 20 | | | | | 25 | | | | | 30 | | |

<210> 64

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<221> VARIANT

<222> 1

<223> X can be either Glu or Asp

<221> VARIANT

<222> 7

<223> X can be either Leu or Ile

<221> VARIANT

<222> 17

<223> X can be either Leu or Ile

<221> VARIANT

<222> 2-3, 5-6, 8-13, 15-16

<223> X can be any amino acid

<400> 64

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Xaa | Xaa | Tyr | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Xaa | Tyr | Xaa |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Xaa | | | | | | | | | | | | | | | |

<210> 65

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<221> VARIANT

<222> 1

<223> X can be either Glu or Asp

<221> VARIANT

<222> 7

<223> X can be either Leu or Ile

<221> VARIANT
<222> 18
<223> X can be either Leu or Ile

<221> VARIANT
<222> 2-3, 5-6, 8-14, 16-17
<223> X can be any amino acid

<400> 65
Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr
1 5 10 15
Xaa Xaa

<210> 66
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<221> VARIANT
<222> 1
<223> X can be either Glu or Asp

<221> VARIANT
<222> 7
<223> X can be either Leu or Ile

<221> VARIANT
<222> 19
<223> X can be either Leu or Ile

<221> VARIANT
<222> 2-3, 5-6, 8-15, 17-18
<223> X can be any amino acid

<400> 66
Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Tyr Xaa Xaa

<210> 67
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
synthetic construct

<221> VARIANT
<222> 1
<223> X can be either Ile or Val or Leu or Ser

<221> VARIANT
<222> 2, 4-5
<223> X can be any amino acid

<221> VARIANT

<222> 6

<223> X can be Leu or Val

<400> 67

Xaa Xaa Tyr Xaa Xaa Xaa
 1 5

<210> 68

<211> 492

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 68

Asp Trp Leu Ser Ile Ser Leu Pro His Arg Ser Tyr Glu Gly Asp Gln
 1 5 10 15
 Val Val Ile Ser Cys Thr Gly Lys Asn Asn Gly Asp Ile Lys Arg Leu
 20 25 30
 Lys Tyr Phe Lys Asp Gly Tyr His Ile Glu Thr Tyr Ser Ser Ala Ser
 35 40 45
 Ser Tyr Thr Ile Arg Asn Ala Arg Arg Gly Asp Ser Gly Ser Tyr Ser
 50 55 60
 Cys Lys Ala Asp Arg Lys Phe Phe Leu Phe Ile Asp Thr Thr Glu Glu
 65 70 75 80
 Thr Gly Ser Lys Trp Leu Asn Val Gln Glu Leu Phe Pro Ala Pro Gly
 85 90 95
 Leu Thr Ala Ser Pro Leu Gln Pro Val Glu Gly Ser Ser Val Thr Leu
 100 105 110
 Ser Cys Asn Thr Trp Leu Pro Ser Asp Arg Ala Thr Thr Gln Leu Arg
 115 120 125
 Tyr Ser Phe Phe Lys Asp Gly His Thr Leu Gln Ser Gly Trp Thr Ser
 130 135 140
 Ser Lys Phe Thr Ile Ser Ala Ile Ser Lys Glu Asp Ser Gly Asn Tyr
 145 150 155 160
 Trp Cys Glu Ala Met Thr Ala Ser Arg Ser Val Ser Lys Gln Ser His
 165 170 175
 Arg Ser Tyr Ile Asp Val Glu Arg Ile Pro Val Ser Gln Val Thr Met
 180 185 190
 Glu Ile Gln Pro Ser Arg Gly Trp Gly Val Glu Gly Glu Pro Leu Val
 195 200 205
 Val Glu Gly Glu Pro Leu Val Leu Ala Cys Ser Val Ala Lys Gly Thr
 210 215 220
 Gly Leu Ile Thr Phe Ser Trp His Arg Gln Asp Thr Lys Glu Ser Val
 225 230 235 240
 Gly Lys Lys Ser Gln Arg Ser Gln Arg Val Glu Leu Glu Ile Pro Thr
 245 250 255
 Ile Arg Glu Ser His Ala Gly Gly Tyr Tyr Cys Thr Ala Asp Asn Asn
 260 265 270
 Tyr Gly Leu Ile Gln Ser Ala Ile Val Asn Ile Thr Val Lys Ile Pro
 275 280 285
 Val Leu Asn Pro Leu Leu Ser Ile Ser Val Pro Gly Val Leu Pro Phe
 290 295 300
 Ile Gly Asp Val Ala Glu Leu His Cys Glu Asp Lys Arg Ala Ser Pro
 305 310 315 320
 Pro Val Leu Tyr Trp Phe Tyr His Glu Asn Ile Thr Leu Ala Asn Thr

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          325          330          335
Ser Ala Pro Phe Gly Gly Lys Ala Ser Phe Lys Leu Ser Leu Thr Ala
          340          345          350
Gly His Ser Gly Asn Tyr Ser Cys Glu Ala Glu Asn Ala Trp Gly Thr
          355          360          365
Lys Arg Ser Glu Val Val Thr Leu Asn Val Thr Glu Pro Pro Pro Lys
          370          375          380
Val Arg Leu Val Asn Gly Pro His His Cys Glu Gly Arg Val Glu Val
          385          390          395          400
Glu Gln Glu Gly Arg Trp Gly Thr Val Cys Asp Asp Gly Trp Asp Met
          405          410          415
Arg Asp Val Ala Val Val Cys Arg Glu Leu Gly Cys Gly Ala Ala Gln
          420          425          430
His Thr Pro Ile Ala Met Leu Tyr Pro Pro Ala Val Asp Glu Ala Leu
          435          440          445
Pro Val Leu Ile Gln Val Ala Leu Cys Asn Gly Thr Glu Lys Thr Leu
          450          455          460
Ala Glu Cys Asp Gln Val Glu Ala Phe Asp Cys Gly His Asp Glu Asp
          465          470          475          480
Ala Gly Ala Val Cys Glu Val Leu Pro Ser Thr Phe
          485          490

```

<210> 69
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 69
 Met Pro Leu Cys Leu Leu Leu Leu Val Phe Ala Pro Val Gly Val Gln
 1 5 10 15
 Ser

<210> 70
 <211> 383
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 70
 Asp Trp Leu Ser Ile Ser Leu Pro His Arg Ser Tyr Glu Gly Asp Gln
 1 5 10 15
 Val Val Ile Ser Cys Thr Gly Lys Asn Asn Gly Asp Ile Lys Arg Leu
 20 25 30
 Lys Tyr Phe Lys Asp Gly Tyr His Ile Glu Thr Tyr Ser Ser Ala Ser
 35 40 45
 Ser Tyr Thr Ile Arg Asn Ala Arg Arg Gly Asp Ser Gly Ser Tyr Ser
 50 55 60
 Cys Lys Ala Asp Arg Lys Phe Phe Leu Phe Ile Asp Thr Thr Glu Glu
 65 70 75 80
 Thr Gly Ser Lys Trp Leu Asn Val Gln Glu Leu Phe Pro Ala Pro Gly
 85 90 95
 Leu Thr Ala Ser Pro Leu Gln Pro Val Glu Gly Ser Ser Val Thr Leu
 100 105 110

Ser Cys Asn Thr Trp Leu Pro Ser Asp Arg Ala Thr Thr Gln Leu Arg
 115 120 125
 Tyr Ser Phe Phe Lys Asp Gly His Thr Leu Gln Ser Gly Trp Thr Ser
 130 135 140
 Ser Lys Phe Thr Ile Ser Ala Ile Ser Lys Glu Asp Ser Gly Asn Tyr
 145 150 155 160
 Trp Cys Glu Ala Met Thr Ala Ser Arg Ser Val Ser Lys Gln Ser His
 165 170 175
 Arg Ser Tyr Ile Asp Val Glu Arg Ile Pro Val Ser Gln Val Thr Met
 180 185 190
 Glu Ile Gln Pro Ser Arg Gly Trp Gly Val Glu Gly Glu Pro Leu Val
 195 200 205
 Val Glu Gly Glu Pro Leu Val Leu Ala Cys Ser Val Ala Lys Gly Thr
 210 215 220
 Gly Leu Ile Thr Phe Ser Trp His Arg Gln Asp Thr Lys Glu Ser Val
 225 230 235 240
 Gly Lys Lys Ser Gln Arg Ser Gln Arg Val Glu Leu Glu Ile Pro Thr
 245 250 255
 Ile Arg Glu Gly His Ala Gly Gly Tyr Tyr Cys Thr Ala Asp Asn Asn
 260 265 270
 Tyr Gly Leu Ile Gln Ser Ala Ile Val Asn Ile Thr Val Lys Ile Pro
 275 280 285
 Val Leu Asn Pro Leu Leu Ser Ile Ser Val Pro Gly Val Leu Pro Phe
 290 295 300
 Ile Gly Asp Val Ala Glu Leu His Cys Glu Asp Lys Arg Ala Ser Pro
 305 310 315 320
 Pro Val Leu Tyr Trp Phe Tyr His Glu Asn Ile Thr Leu Ala Asn Thr
 325 330 335
 Ser Ala Pro Phe Gly Gly Lys Ala Ser Phe Lys Leu Ser Leu Thr Ala
 340 345 350
 Gly His Ser Gly Asn Tyr Ser Cys Glu Ala Glu Asn Ala Trp Gly Thr
 355 360 365
 Lys Arg Ser Glu Val Val Thr Leu Asn Val Thr Gly Arg Thr Ile
 370 375 380

<210> 71

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 71

Met Pro Leu Cys Leu Leu Leu Val Phe Ala Pro Val Gly Val Gln
 1 5 10 15
 Ser

<210> 72

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 72

Met Leu Pro Trp Leu Leu Leu Leu Ile Cys Ala Leu Pro Cys Glu Pro
 1 5 10 15
 Ala

<210> 73
 <211> 326
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 73
 Gly Ile Ser Asp Val Ser Leu Lys Thr Arg Pro Pro Gly Gly Trp Val
 1 5 10 15
 Met Glu Gly Asp Lys Leu Val Leu Ile Cys Ser Val Asp Arg Val Thr
 20 25 30
 Gly Asn Ile Thr Tyr Phe Trp Tyr Arg Gly Ala Leu Gly Phe Gln Leu
 35 40 45
 Glu Thr Lys Thr Gln Pro Ser Leu Thr Ala Glu Phe Glu Ile Ser Asp
 50 55 60
 Met Lys Gln Ser Asp Ala Asp Gln Tyr Tyr Cys Ala Ala Asn Asp Gly
 65 70 75 80
 His Asp Pro Ile Ala Ser Glu Leu Val Ser Ile His Val Arg Val Pro
 85 90 95
 Val Ser Arg Pro Val Leu Thr Phe Gly Asp Ser Gly Thr Gln Ala Val
 100 105 110
 Leu Gly Asp Leu Val Glu Leu His Cys Lys Ala Leu Arg Gly Ser Pro
 115 120 125
 Pro Ile Phe Tyr Gln Phe Tyr His Glu Ser Ile Ile Leu Gly Asn Ser
 130 135 140
 Ser Ala Pro Ser Gly Gly Ala Ser Phe Asn Phe Ser Leu Thr Ala
 145 150 155 160
 Glu His Ser Gly Asn Phe Ser Cys Glu Ala Ser Asn Gly Gln Gly Ala
 165 170 175
 Gln Arg Ser Glu Val Val Ala Leu Asn Leu Thr Gly Leu Ser Leu Val
 180 185 190
 Pro Thr Glu Asn Gly Ile Ser His Leu Ser Leu Gly Leu Thr Gly Trp
 195 200 205
 Leu Leu Gly Cys Leu Ser Pro Ile Thr Met Ala Leu Ile Phe Cys Tyr
 210 215 220
 Trp Leu Lys Arg Lys Ile Gly Arg Gln Ser Glu Asp Pro Val Arg Ser
 225 230 235 240
 Pro Pro Gln Thr Val Leu Gln Gly Ser Thr Tyr Pro Lys Ser Pro Asp
 245 250 255
 Ser Arg Gln Pro Glu Pro Leu Tyr Glu Asn Val Asn Val Val Ser Gly
 260 265 270
 Asn Glu Val Tyr Ser Leu Val Tyr His Thr Pro Gln Val Leu Glu Pro
 275 280 285
 Ala Ala Ala Gln His Val Arg Thr His Gly Val Ser Glu Ser Phe Gln
 290 295 300
 Val Ser Ser Gly Leu Tyr Ser Lys Pro Arg Ile Asn Ile Ala His Met
 305 310 315 320
 Asp Tyr Glu Asp Ala Met
 325

<210> 74
 <211> 203
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 74

```

Gly Ile Ser Asp Val Ser Leu Lys Thr Arg Pro Pro Gly Gly Trp Val
 1           5           10           15
Met Glu Gly Asp Lys Leu Val Leu Ile Cys Ser Val Asp Arg Val Thr
          20           25           30
Gly Asn Ile Thr Tyr Phe Trp Tyr Arg Gly Ala Leu Gly Phe Gln Leu
          35           40           45
Glu Thr Lys Thr Gln Pro Ser Leu Thr Ala Glu Phe Glu Ile Ser Asp
          50           55           60
Met Lys Gln Ser Asp Ala Asp Gln Tyr Tyr Cys Ala Ala Asn Asp Gly
65           70           75           80
His Asp Pro Ile Ala Ser Glu Leu Val Ser Ile His Val Arg Val Pro
          85           90           95
Val Ser Arg Pro Val Leu Thr Phe Gly Asp Ser Gly Thr Gln Ala Val
          100          105          110
Leu Gly Asp Leu Val Glu Leu His Cys Lys Ala Leu Arg Gly Ser Pro
          115          120          125
Pro Ile Phe Tyr Gln Phe Tyr His Glu Ser Ile Ile Leu Gly Asn Ser
          130          135          140
Ser Ala Pro Ser Gly Gly Gly Ala Ser Phe Asn Phe Ser Leu Thr Ala
          145          150          155          160
Glu His Ser Gly Asn Phe Ser Cys Glu Ala Ser Asn Gly Gln Gly Ala
          165          170          175
Gln Arg Ser Glu Val Val Ala Leu Asn Leu Thr Gly Leu Ser Leu Val
          180          185          190
Pro Thr Glu Asn Gly Ile Ser His Leu Ser Leu
          195          200

```

<210> 75

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 75

```

Met Leu Pro Trp Leu Leu Leu Ile Cys Ala Leu Pro Cys Glu Pro
 1           5           10           15
Ala

```

<210> 76

<211> 100

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 76

```

Lys Arg Lys Ile Gly Arg Gln Ser Glu Asp Pro Val Arg Ser Pro Pro
 1           5           10           15

```

Gln Thr Val Leu Gln Gly Ser Thr Tyr Pro Lys Ser Pro Asp Ser Arg
 20 25 30
 Gln Pro Glu Pro Leu Tyr Glu Asn Val Asn Val Val Ser Gly Asn Glu
 35 40 45
 Val Tyr Ser Leu Val Tyr His Thr Pro Gln Val Leu Glu Pro Ala Ala
 50 55 60
 Ala Gln His Val Arg Thr His Gly Val Ser Glu Ser Phe Gln Val Ser
 65 70 75 80
 Ser Gly Leu Tyr Ser Lys Pro Arg Ile Asn Ile Ala His Met Asp Tyr
 85 90 95
 Glu Asp Ala Met
 100

<210> 77
 <211> 283
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 77
 Gly Ile Ser Asp Val Ser Leu Lys Thr Arg Pro Pro Gly Gly Trp Val
 1 5 10 15
 Met Glu Gly Asp Lys Leu Val Leu Ile Cys Ser Val Asp Arg Val Thr
 20 25 30
 Gly Asn Ile Thr Tyr Phe Trp Tyr Arg Gly Ala Leu Gly Phe Gln Leu
 35 40 45
 Glu Thr Lys Thr Gln Pro Ser Leu Thr Ala Glu Phe Glu Ile Ser Asp
 50 55 60
 Met Lys Gln Ser Asp Ala Asp Gln Tyr Tyr Cys Ala Ala Asn Asp Gly
 65 70 75 80
 His Asp Pro Ile Ala Ser Glu Leu Val Ser Ile His Val Arg Val Pro
 85 90 95
 Val Ser Arg Pro Val Leu Thr Phe Gly Asp Ser Gly Thr Gln Ala Val
 100 105 110
 Leu Gly Asp Leu Val Glu Leu His Cys Lys Ala Leu Arg Gly Ser Pro
 115 120 125
 Pro Ile Phe Tyr Gln Phe Tyr His Glu Ser Ile Ile Leu Gly Asn Ser
 130 135 140
 Ser Ala Pro Ser Gly Gly Gly Ala Ser Phe Asn Phe Ser Leu Thr Ala
 145 150 155 160
 Glu His Ser Gly Asn Phe Ser Cys Glu Ala Ser Asn Gly Gln Gly Ala
 165 170 175
 Gln Arg Ser Glu Val Val Ala Leu Asn Leu Thr Gly Arg Gln Ser Glu
 180 185 190
 Asp Pro Val Arg Ser Pro Pro Gln Thr Val Leu Gln Gly Ser Thr Tyr
 195 200 205
 Pro Lys Ser Pro Asp Ser Arg Gln Pro Glu Pro Leu Tyr Glu Asn Val
 210 215 220
 Asn Val Val Ser Gly Asn Glu Val Tyr Ser Leu Val Tyr His Thr Pro
 225 230 235 240
 Gln Val Leu Glu Pro Ala Ala Ala Gln His Val Arg Thr His Gly Val
 245 250 255
 Ser Glu Ser Phe Gln Val Ser Ser Gly Leu Tyr Ser Lys Pro Arg Ile
 260 265 270
 Asn Ile Ala His Met Asp Tyr Glu Asp Ala Met
 275 280

<210> 78

<211> 570
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 78

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gln | His | Glu | Ala | Ala | Gln | Gln | Ser | Val | Val | Ser | Leu | Gln | Pro | Pro | 1 | 5 | 10 | 15 |
| Trp | Thr | Thr | Phe | Phe | Arg | Gly | Glu | Val | Val | Thr | Leu | Thr | Cys | Tyr | Arg | 20 | 25 | 30 | |
| Phe | Gly | Phe | Ser | Val | Pro | Gln | Lys | Thr | Lys | Trp | Tyr | Gln | Lys | Arg | Lys | 35 | 40 | 45 | |
| Thr | Val | Lys | Gln | Thr | Pro | Gly | Ala | Leu | Val | Ile | Lys | Ala | His | Thr | Leu | 50 | 55 | 60 | |
| Lys | Val | His | Glu | Ser | Gly | Glu | Tyr | Trp | Cys | Gln | Ala | Asp | Ser | Leu | Leu | 65 | 70 | 75 | 80 |
| Pro | Ser | Met | His | Val | Asn | Val | Glu | Phe | Ser | Glu | Asp | Phe | Leu | Val | Leu | 85 | 90 | 95 | |
| Gln | Ala | Pro | Pro | Ala | Val | Phe | Glu | Gly | Asp | Ser | Val | Val | Leu | Arg | Cys | 100 | 105 | 110 | |
| Tyr | Ala | Lys | Lys | Gly | Ile | Glu | Ala | Glu | Thr | Leu | Thr | Phe | Tyr | Lys | Asp | 115 | 120 | 125 | |
| Gly | Lys | Ala | Leu | Thr | Leu | His | His | Gln | Ser | Glu | Leu | Ser | Ile | His | His | 130 | 135 | 140 | |
| Ala | Asn | Leu | Lys | Asp | Asn | Gly | Gln | Tyr | Lys | Cys | Thr | Ser | Lys | Lys | Lys | 145 | 150 | 155 | 160 |
| Trp | Ser | Phe | Gly | Ser | Leu | Tyr | Thr | Ser | Asn | Thr | Val | Gly | Val | Gln | Val | 165 | 170 | 175 | |
| Gln | Glu | Leu | Phe | Pro | Arg | Pro | Val | Leu | Arg | Ala | Arg | Pro | Ser | His | Pro | 180 | 185 | 190 | |
| Ile | Asp | Gly | Ser | Pro | Val | Thr | Leu | Thr | Cys | Gln | Thr | Gln | Leu | Ser | Ala | 195 | 200 | 205 | |
| Gln | Lys | Ser | Asp | Ala | Arg | Leu | Gln | Phe | Cys | Phe | Phe | Arg | Asn | Leu | Gln | 210 | 215 | 220 | |
| Leu | Leu | Gly | Ser | Gly | Cys | Ser | Arg | Ser | Ser | Glu | Phe | His | Ile | Pro | Ala | 225 | 230 | 235 | 240 |
| Ile | Trp | Thr | Glu | Glu | Ser | Arg | Arg | Tyr | Gln | Cys | Lys | Ala | Glu | Thr | Val | 245 | 250 | 255 | |
| Asn | Ser | Gln | Val | Arg | Lys | Gln | Ser | Thr | Ala | Phe | Ile | Ile | Pro | Val | Gln | 260 | 265 | 270 | |
| Arg | Ala | Ser | Ala | Arg | Phe | Gln | Thr | His | Ile | Ile | Pro | Ala | Ser | Lys | Leu | 275 | 280 | 285 | |
| Val | Phe | Glu | Gly | Gln | Leu | Leu | Leu | Asn | Cys | Ser | Val | Lys | Gly | Val | | 290 | 295 | 300 | |
| Pro | Gly | Pro | Leu | Lys | Phe | Ser | Trp | Tyr | Lys | Lys | Asp | Met | Leu | Asn | Glu | 305 | 310 | 315 | 320 |
| Glu | Thr | Lys | Ile | Leu | Lys | Ser | Ser | Asn | Ala | Glu | Phe | Lys | Ile | Ser | Gln | 325 | 330 | 335 | |
| Val | Asn | Ile | Ser | Asp | Ala | Gly | Glu | Tyr | His | Cys | Glu | Ala | Thr | Asn | Ser | 340 | 345 | 350 | |
| Arg | Arg | Ser | Phe | Val | Ser | Arg | Ala | Phe | Pro | Ile | Thr | Ile | Lys | Val | Pro | 355 | 360 | 365 | |
| Val | Ser | Gln | Pro | Val | Leu | Thr | Leu | Ser | Thr | Gly | Lys | Thr | Gln | Ala | Leu | 370 | 375 | 380 | |
| Glu | Gly | Asp | Leu | Met | Thr | Leu | His | Cys | Gln | Ser | Gln | Arg | Gly | Ser | Pro | 385 | 390 | 395 | 400 |
| Cys | Ile | Leu | Tyr | Glu | Phe | Phe | Tyr | Glu | Asn | Val | Ser | Leu | Gly | Asn | Ser | 405 | 410 | 415 | |

```

Ser Ile Leu Ser Gly Gly Gly Ala Tyr Phe Asn Phe Ser Met Ser Thr
      420      425
Glu Arg Ser Gly Asn Tyr Tyr Cys Thr Ala Asp Asn Gly Leu Gly Ala
      435      440      445
Gln Cys Ser Glu Ala Ile Arg Ile Ser Ile Phe Asp Met Thr Lys Asn
      450      455      460
Arg Ser Val Pro Met Ala Ala Gly Ile Thr Val Gly Leu Leu Ile Met
465      470      475
Ala Val Gly Val Phe Leu Phe Tyr Cys Trp Phe Ser Arg Lys Ala Gly
      485      490      495
Gly Lys Pro Thr Ser Asp Asp Ser Arg Asn Pro Ser Asp Ser Glu Pro
      500      505      510
Gln Glu Pro Thr Tyr Tyr Asn Val Pro Ala Cys Ile Glu Leu Gln Pro
      515      520      525
Val Tyr Ser Asn Glu Pro Glu Glu Asn Val Ile Tyr Thr Glu Val Arg
      530      535      540
Arg Thr Gln Pro Arg Gln Lys His Ala Asp Gln Glu Ser Glu Ser Pro
545      550      555      560
Arg Ser Arg Cys Gln Met Ala Glu Lys Lys
      565      570

```

<210> 79
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

```

<400> 79
Met Ser Gly Ser Phe Ser Pro Cys Val Val Phe Thr Gln Met Trp Leu
  1      5      10      15
Thr Leu Leu Val Val Thr Pro Val Asn
      20      25

```

<210> 80
 <211> 468
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

```

<400> 80
Gly Gln His Glu Ala Ala Gln Gln Ser Val Val Ser Leu Gln Pro Pro
  1      5      10      15
Trp Thr Thr Phe Phe Arg Gly Glu Val Val Thr Leu Thr Cys Tyr Arg
      20      25      30
Phe Gly Phe Ser Val Pro Gln Lys Thr Lys Trp Tyr Gln Lys Arg Lys
      35      40      45
Thr Val Lys Gln Thr Pro Gly Ala Leu Val Ile Lys Ala His Thr Leu
      50      55      60
Lys Val His Glu Ser Gly Glu Tyr Trp Cys Gln Ala Asp Ser Leu Leu
65      70      75      80
Pro Ser Met His Val Asn Val Glu Phe Ser Glu Asp Phe Leu Val Leu
      85      90      95
Gln Ala Pro Pro Ala Val Phe Glu Gly Asp Ser Val Val Leu Arg Cys
      100      105      110

```

Tyr Ala Lys Lys Gly Ile Glu Ala Glu Thr Leu Thr Phe Tyr Lys Asp
 115 120 125
 Gly Lys Ala Leu Thr Leu His Gln Ser Glu Leu Ser Ile His His
 130 135 140
 Ala Asn Leu Lys Asp Asn Gly Gln Tyr Lys Cys Thr Ser Lys Lys Lys
 145 150 155 160
 Trp Ser Phe Gly Ser Leu Tyr Thr Ser Asn Thr Val Gly Val Gln Val
 165 170 175
 Gln Glu Leu Phe Pro Arg Pro Val Leu Arg Ala Arg Pro Ser His Pro
 180 185 190
 Ile Asp Gly Ser Pro Val Thr Leu Thr Cys Gln Thr Gln Leu Ser Ala
 195 200 205
 Gln Lys Ser Asp Ala Arg Leu Gln Phe Cys Phe Phe Arg Asn Leu Gln
 210 215 220
 Leu Leu Gly Ser Gly Cys Ser Arg Ser Ser Glu Phe His Ile Pro Ala
 225 230 235 240
 Ile Trp Thr Glu Glu Ser Arg Arg Tyr Gln Cys Lys Ala Glu Thr Val
 245 250 255
 Asn Ser Gln Val Arg Lys Gln Ser Thr Ala Phe Ile Ile Pro Val Gln
 260 265 270
 Arg Ala Ser Ala Arg Phe Gln Thr His Ile Ile Pro Ala Ser Lys Leu
 275 280 285
 Val Phe Glu Gly Gln Leu Leu Leu Leu Asn Cys Ser Val Lys Gly Val
 290 295 300
 Pro Gly Pro Leu Lys Phe Ser Trp Tyr Lys Lys Asp Met Leu Asn Glu
 305 310 315 320
 Glu Thr Lys Ile Leu Lys Ser Ser Asn Ala Glu Phe Lys Ile Ser Gln
 325 330 335
 Val Asn Ile Ser Asp Ala Gly Glu Tyr His Cys Glu Ala Thr Asn Ser
 340 345 350
 Arg Arg Ser Phe Val Ser Arg Ala Phe Pro Ile Thr Ile Lys Val Pro
 355 360 365
 Val Ser Gln Pro Val Leu Thr Leu Ser Thr Gly Lys Thr Gln Ala Leu
 370 375 380
 Glu Gly Asp Leu Met Thr Leu His Cys Gln Ser Gln Arg Gly Ser Pro
 385 390 395 400
 Cys Ile Leu Tyr Glu Phe Phe Tyr Glu Asn Val Ser Leu Gly Asn Ser
 405 410 415
 Ser Ile Leu Ser Gly Gly Gly Ala Tyr Phe Asn Phe Ser Met Ser Thr
 420 425 430
 Glu Arg Ser Gly Asn Tyr Tyr Cys Thr Ala Asp Asn Gly Leu Gly Ala
 435 440 445
 Gln Cys Ser Glu Ala Ile Arg Ile Ser Ile Phe Asp Met Thr Lys Asn
 450 455 460
 Arg Ser Val Pro
 465

<210> 81

<211> 79

<212> PRT

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 81

Ser Arg Lys Ala Gly Gly Lys Pro Thr Ser Asp Asp Ser Arg Asn Pro
 1 5 10 15
 Ser Asp Ser Glu Pro Gln Glu Pro Thr Tyr Tyr Asn Val Pro Ala Cys
 20 25 30

```

Ile Glu Leu Gln Pro Val Tyr Ser Asn Glu Pro Glu Glu Asn Val Ile
      35              40              45
Tyr Thr Glu Val Arg Arg Thr Gln Pro Arg Gln Lys His Ala Asp Gln
      50              55              60
Glu Ser Glu Ser Pro Arg Ser Arg Cys Gln Met Ala Glu Lys Lys
      65              70              75

```

<210> 82
 <211> 1973
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

```

<400> 82
ccacagtgtt ctatcccaga tccgtggtcc atctgcccta aggacttgag ctgcacctgt      60
ctcaaaggga gctacttgcc tctagtctca tgccctctgtg cttgctgctt ctgggtcttcg      120
ctcctgtcgg agtccagtcg gactggttga gcatcagcct tccacaccgt tcttatgaag      180
gagaccaagt agttataaag tgcaacaggaa aaaataatgg tgacataaag agactgaagt      240
acttcaagga tggatatcac atagaaaactt acagcagtgcc ttcaagctac accattagga      300
atgcaagacg tgggtgacagt ggctcctatt cctgtaaggc agataggaaa tttttcctat      360
ttatagacac aacagaagaa acaggatcta agtggctgaa tgtccaagag ctgtttccag      420
cacctgggct gacagccagc cccctgcagc ccgtagaggg gagttcagtg accctgtcct      480
gcaacacctg gctcccttca gatagggcaa cgacccagct acgctattcc ttcttcaaag      540
atggccacac tttgcaatcg ggctggacct catcaaaatt taccatctca gcaatatcga      600
aggaagactc aggaaattac tgggtgtgaag caatgactgc ctctgcagtg gtctcaaagc      660
agagtcaccg gtcctacata gatgtagaga ggatccctgt atctcaagtc accatggaaa      720
tccagccttc aaggggctgg ggagttgaag gggagccact ggtcgttgaa ggggagcccc      780
tggtcctggc ttgtttctgtg gctaaaggca ccgggctaata cactgtatgt accatggaaa      840
aggacactaa ggaaagtgtg gggaagaaaa gtcagcgttc ccagagagtg gagctggaga      900
tccctactat caggggaaggc catgctgggg ggtactactg cacagcagac aacaactacg      960
gcctgatcca gagcgcaatc gtgaacatca ccgtgaaaaat tccagtgttg aaccogctcc      1020
tctccatcag tgttccctggg gtcttgcctt tcctcggaga tgtggcggag cttcactgtg      1080
aagacaagag agcatctcct ccggttctct actggtttta tcatgaaaat atcactctgg      1140
ctaacaacctc ggcaaccttt ggaggaaagg catcctttta gctctctctg actgcagggc      1200
attctgggaa ctactcttgt gaggctgaaa acgcctgggg taccaagcgc agtgagggtg      1260
taacgctcaa tgccacagag cccccaccca aagtgcgttt ggtgaatggc ccccaacct      1320
gtgaaggacg cgtagagggtg gagcaggaag gtcgctgggg cactgtatgt gatgatggct      1380
gggacatgag ggatgtggct gtggtgtgcc gagagctggg ctgtggagca gcccaacaca      1440
cacctatagc catgctgtat ccaccagcag ttgatgaagc tctgcctgtg ctcatcagg      1500
tagcctgtg caatggcaca gaaaagaccc tggctgaatg tgaccaggtt gaggcctttg      1560
attgtggaca tgatgaggat gctggagctg tgtgtgaagt cttaccagc acttttctgaa      1620
gatctagaga ccagagacca tcagacctcc tactttctgc actgggcctc acagccctca      1680
cggtctgcag ctcccagtg acttccagac ttcagctgtg gcttatcctt caagaggact      1740
cgaaactata ttaatctgct ctgagataat gttccaacag ctccaaagaa agcccagatc      1800
ccttgtcccc agaggccaag cttggaaaaa ttgttcccct gtccagggtc cctgcctttc      1860
tagttccttc ttgctatctc cttgggcaga tgcagaggtg gcacaagtaa ggatcacata      1920
catgtgcctg ggcttccatc tggtagaatg tgggtctaaca aagcacatac aac      1973

```

<210> 83
 <211> 1530
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

<400> 83

| | | | | | | |
|------------|-------------|-------------|-------------|-------------|-------------|------|
| atgcctctgt | gcttgcctgt | tctgggtcttc | gctcctgtcg | gagtcacagtc | cgactgggttg | 60 |
| agcatcagcc | ttccacacccg | ttcttatgaa | ggagaccaag | tagttataag | ctgcacagga | 120 |
| aaaaataatg | gtgacataaa | gagactgaag | tacttcaagg | atggatatca | catagaaact | 180 |
| tacagcagtg | cttcaagcta | caccattagg | aatgcaagac | gtggtagacag | tggtctctat | 240 |
| tcctgtaagg | cagataggaa | atcttttcta | tttatagaca | caacagaaga | aacaggatct | 300 |
| aagtggctga | atgtccaaga | gctgtttcca | gcacctgggc | tgacagccag | ccccctgcag | 360 |
| cccgtagagg | ggagttcagt | gacctgtgoc | tgcaacacct | ggctcccttc | agatagggca | 420 |
| acgacccagc | tacgctattc | cttcttcaaa | gatggccaca | ctttgcaatc | gggctggacc | 480 |
| tcatcaaaat | ttaccatctc | agcaatatcg | aaggaagact | caggaaatta | ctgggtgtgaa | 540 |
| gcaatgactg | cctctcgag | tgtctcaaag | cagagtcacc | ggtcctacat | agatgtagag | 600 |
| aggatccctg | tatctcaagt | cacccatggaa | atccagcctt | caaggggctg | gggagttgaa | 660 |
| ggggagccac | tggtcggtga | aggggagccc | ctggctcctgg | cttggttctgt | ggctaaaggc | 720 |
| accgggctaa | tcacgttctc | ctggcatagg | caggacacta | aggaaagtgt | ggggaagaaa | 780 |
| agtcagcgtt | cccagagagt | ggagctggag | atccctacta | tcagggaagg | ccatgctggg | 840 |
| gggtactact | gcacagcaga | caacaactac | ggcctgatcc | agagcgcaat | cgtgaacatc | 900 |
| accgtgaaaa | ttccagtgtt | gaaccgcctc | ctctccatca | gtgttcctgg | ggtcttgccc | 960 |
| ttcatcggag | atgtggcgga | gcttcaactgt | gaagacaaga | gagcatctcc | tccggttctc | 1020 |
| tactggtttt | atcatgaaaa | tatcactctg | gctaacacct | cggcaccttt | tggaggaaaag | 1080 |
| gcatecttta | agctctctct | gactgcaggg | cattctggga | actactcttg | tgaggctgaa | 1140 |
| aacgcctggg | gtaccaagcg | cagtgcaggtg | gtaacgctca | atgtcacaga | gccccacccc | 1200 |
| aaagtgcgtt | tggtgaatgg | ccccaccac | tgtgaaggac | gcgtagagggt | ggagcaggaa | 1260 |
| ggtcgctggg | gcactgtatg | tgatgatggc | tgggacatga | gggatgtggc | tgtgggtgtgc | 1320 |
| cgagagctgg | gctgtggagc | agcccaacac | acacctatag | ccatgctgta | tccaccagca | 1380 |
| gttgatgaag | ctctgcctgt | gctcattcag | gtagccctgt | gcaatggcac | agaaaagacc | 1440 |
| ctggctgaat | gtgaccaggt | tgaggccttt | gattgtggac | atgatgagga | tgctggagct | 1500 |
| gtgtgtgaag | tcttaccag | cactttctga | | | | 1530 |

<210> 84

<211> 1371

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 84

| | | | | | | |
|------------|------------|-------------|-------------|-------------|-------------|------|
| ccacagtgtt | ctatcccaga | tccgtgggtcc | atctgcccta | aggacttgag | ctgcacctgt | 60 |
| ctcaaaggga | gctacttgcc | tctagtctca | tgcctctgtg | cttgctgctt | ctggctcttcg | 120 |
| ctcctgtcgg | agtccagtc | gactgggtga | gcatcagcct | tccacaccgt | tcttatgaag | 180 |
| gagaccaagt | agttataagc | tgcaacaggaa | aaaataatgg | tgacataaag | agactgaagt | 240 |
| acttcaagga | tgatattcac | atagaaactt | acagcagtg | ttcaagctac | accattagga | 300 |
| atgcaagacg | tggtgacagt | ggctcctatt | cctgtaaggc | agataggaaa | tttttcctat | 360 |
| ttatagacac | aacagaagaa | acaggatcta | agtggctgaa | tgtccaagag | ctgtttccag | 420 |
| cacctgggct | gacagccagc | cccctgcagc | ccgtagaggg | gagttcagtg | accctgtcct | 480 |
| gcaacacctg | gctcccttca | gatagggcaa | cgaccagct | acgctattcc | ttcttcaaag | 540 |
| atggccacac | tttgcaatcg | ggctggacct | catcaaaaatt | taccatctca | gcaatatcga | 600 |
| aggaagactc | aggaaattac | tggtgtgaag | caatgactgc | ctctcgcagt | gtctcaaagc | 660 |
| agagtcaccg | gtcctacata | gatgtagaga | ggatccctgt | atctcaagtc | accatggaaa | 720 |
| tccagccttc | aaggggctgg | ggagttgaag | gggagccact | ggtcgttgaa | ggggagcccc | 780 |
| tggtcctggc | ttgttctgtg | gctaaaggca | ccgggcta | caaggttctcc | tggtcataggc | 840 |
| aggacactaa | ggaaagtgtg | gggaagaaaa | gtcagcgttc | ccagagagtg | gagctggaga | 900 |
| tcctactat | cagggaaggc | catgctgggg | ggtactactg | cacagcagac | aacaactacg | 960 |
| gctgatcca | gagcgcaatc | gtgaacatca | ccgtgaaaat | tccagtgttg | aaccgcctcc | 1020 |
| tctccatcag | tggttctggg | gtcttgcctc | tcacgggaga | tgtggcggag | cttcaactgtg | 1080 |
| aagacaagag | agcatctcct | ccgggttctct | actggtttta | tcattgaaaat | atcactcttg | 1140 |
| ctaacacctc | ggcacctttt | ggaggaaaag | catcctttta | gctctctctg | actgcagggc | 1200 |
| attctgggaa | ctactcttgt | gaggctgaaa | acgcctgggg | taccaagcgc | agtgaggtgg | 1260 |
| taacgcctca | tgtcacaggt | aggacaattt | aatgatccat | tccaggggtgc | aacttgcctt | 1320 |
| ctggccatgc | ccttcttctc | tcccttgac | ctgtacctct | tggtctttga | a | 1371 |

<210> 85
 <211> 1203
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

```

<400> 85
atgcctctgt gcttgctgct tctgggtcttc gctcctgtcg gagtccagtc cgactgggttg      60
agcatcagcc ttccacaccg ttcttatgaa ggagaccaag tagttataag ctgcacagga      120
aaaaataatg gtgacataaa gagactgaag tacttcaagg atggatatca catagaaact      180
tacagcagtg cttcaagcta caccattagg aatgcaagac gtggtgacag tggctcctat      240
tcctgtgaagg cagataggaa atttttccta tttatagaca caacagaaga aacaggatct      300
aagtggctga atgtccaaga gctgtttcca gcacctgggc tgacagccag cccctgcag      360
cccgtagagg ggagttcagt gacctgttc tgcaacacct ggctcccttc agatagggca      420
acgacccagc tacgctattc cttcttcaaa gatggccaca ctttgcaatc gggctggacc      480
tcatcaaaat ttaccatctc agcaatatcg aaggaagact caggaaatta ctggtgtgaa      540
gcaatgactg cctctcgagc tgtctcaaag cagagtcacc ggtcctacat agatgtagag      600
aggatccctg tatctcaagt caccatggaa atccagcctt caaggggctg gggagttaga      660
ggggagccac tggctggttg aggggagccc ctggctcctgg caggacacta aggaaagtgt ggggaagaaa      720
accgggctaa tcacgtttctc ctggcatagg caggacacta aggaaagtgt ggggaagaaa      780
agtcagcggt cccagagagt ggagctggag atccctacta tcaggaagg ccattgctggg      840
gggtactact gcacagcaga caacaactac ggcctgatcc agagcgcaat cgtgaacatc      900
accgtgaaaa ttccagtgtt gaaccgcgtc ctctccatca gtgttccttg ggtcctgccc      960
ttcatoggag atgtggcgga gcttactgt gaagacaaga gagcatctcc tccggttctc     1020
tactggtttt atcatgaaaa tatcactctg gctaacacct cggcaccttt tggaggaaaag     1080
gcacccctta agctctctct gactgcaggg cattctggga actactcttg tgaggctgaa     1140
aacgcctggg gtaccaagcg cagtgaggtg gtaacgctca atgtcacagg taggacaatt     1200
taa                                                                1203
  
```

<210> 86
 <211> 1479
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/note =
 synthetic construct

```

<400> 86
gactgggttg gcatcagcct tccacacogt tcttatgaag gagaccaagt agttataagc      60
tgacacaggaa aaaataatgg tgacataaag agactgaagt acttcaagga tggatatcac     120
atagaaactt acagcagtcg ttcaagctac accattagga atgcaagacg tggtgacagt     180
ggctcctatt cctgtaaggc agataggaaa tttttcctat ttatagacac aacagaagaa     240
acaggatcta agtggctgaa tgtccaagag ctgtttccag cacctgggct gacagccagc     300
cccctgcagc ccgtagaggg gatttcagtg accctgtcct gcaacacctg gctcccttca     360
gatagggcaa cgacccagct acgctattcc ttcttcaaag atggccacac ttgcaatcg     420
ggctggacct catcaaaatt taccatctca gcaatatcga aggaagactc aggaaattac     480
tggtgtgaag caatgactgc ctctcgagcgt gtctcaaagc agagtcaccg gtcctacata     540
gatgtagaga ggatccctgt atctcaagtc accatggaaa tccagccttc aaggggctgg     600
ggagttagaag gggagccact ggtcgttgaa ggggagcccc tggctcctggc ttgttctgtg     660
gctaaaggca ccgggctaata cacgttctcc tggcataggc aggacactaa ggaaagtgtg     720
gggaagaaaa gtcagcgttc ccagagagtg gagctggaga tccctactat cagggaaggc     780
catgctgggg ggtactactg cacagcagac aacaactacg gcctgatcca gagcgcaatc     840
gtgaacatca ccgtgaaaaat tccagtgttg aacccgctcc tctccatcag tgttctctgg     900
gtcttggcct tcatcggaga tgtggcggag cttcactgtg aagacaagag agcatctcct     960
ccggttctct actggtttta tcatgaaaat atcactctgg ctaaaccttc ggcacctttt    1020
ggaggaaaag catcctttaa gctctctctg actgcagggc attctgggaa ctactcttgt    1080
gaggctgaaa acgcctgggg taccaagcgc agtgaggtg taacgctcaa tgtcacagag    1140
  
```

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| ccccaccca | aagtgcgttt | ggtgaatggc | ccccaccact | gtgaaggacg | cgtagaggtg | 1200 |
| gagcaggaag | gtcgtctggg | cactgtatgt | gatgatggct | gggacatgag | ggatgtggct | 1260 |
| gtggtgtgcc | gagagctggg | ctgtggagca | gcccacaca | cacctatagc | catgctgtat | 1320 |
| ccaccagcag | ttgatgaagc | tctgcctgtg | ctcattcagg | tagccctgtg | caatggcaca | 1380 |
| gaaaagaccc | tggctgaatg | tgaccagggt | gaggcctttg | attgtggaca | tgatgaggat | 1440 |
| gctggagctg | tgtgtgaagt | cttaccacgc | actttctga | | | 1479 |

<210> 87

<211> 1152

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 87

| | | | | | | |
|-------------|-------------|-------------|-------------|------------|------------|------|
| gactggttga | gcatcagcct | tccacaccgt | tcttatgaag | gagaccaagt | agttataagc | 60 |
| tgacacaggaa | aaaataatgg | tgacataaag | agactgaagt | acttcaagga | tgatatacac | 120 |
| atagaaacttt | acagcagtg | ttcaagctac | accattagga | atgcaagacg | tggtgacagt | 180 |
| ggctcctatt | cctgtaaggc | agataggaaa | tttttccctat | ttatagacac | aacagaagaa | 240 |
| acaggatcta | agtggctgaa | tgtccaagag | ctgtttccag | cacctgggct | gacagccagc | 300 |
| cccctgcagc | ccgtagaggg | gagttcagtg | accctgtcct | gcaacacctg | gctcccttca | 360 |
| gataggggcaa | cgacccagct | acgctattcc | ttcttcaaag | atggccacac | tttgcaatcg | 420 |
| ggctggacct | catcaaaatt | taccatctca | gcaatatoga | aggaagactc | aggaaattac | 480 |
| tggtgtgaag | caatgactgc | ctctcgagct | gtctcaaagc | agagtcaccg | gtcctacata | 540 |
| gatgtagaga | ggatocctgt | atctcaagtc | accatggaaa | tccagccttc | aaggggctgg | 600 |
| ggagttgaag | gggagccact | ggtcgttgaa | ggggagcccc | tggtcctggc | ttgttctgtg | 660 |
| gctaaaggca | ccgggctaata | cacgttctcc | tgccataggc | aggacactaa | ggaaagtgtg | 720 |
| gggaagaaaa | gtcagcgttc | ccagagagtg | gagctggaga | tccctactat | cagggaaggc | 780 |
| catgctgggg | ggtactactg | cacagcagac | aacaactacg | gcctgatcca | gagcgcaatc | 840 |
| gtgaacatca | ccgtgaaaat | tccagtgttg | aaccgcctcc | tctccatcag | tgttcctggg | 900 |
| gtcttgccct | tcatcggaga | tggtggcggag | cttactgtg | aagacaagag | agcatctcct | 960 |
| ccggttctct | actggtttta | tcatgaaaat | atcactctgg | ctaacacctc | ggcacctttt | 1020 |
| ggaggaaagg | catcctttta | gctctctctg | actgcagggc | attctgggaa | ctactcttgt | 1080 |
| gaggctgaaa | acgcctgggg | taccaagcgc | agtgaggtgg | taacgctcaa | tgtcacaggt | 1140 |
| aggacaattt | aa | | | | | 1152 |

<210> 88

<211> 1567

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 88

| | | | | | | |
|-------------|------------|------------|-------------|-------------|------------|-----|
| tgagtagtct | ggttttgctt | ttttttcttt | tggtgagagg | taccttcaag | ttaccatccc | 60 |
| cagcctgggc | ctcatgctac | cttggctcct | gctactgato | tggtgctctac | cgtgtgaacc | 120 |
| tgctggaatc | tctgatgtga | gcttgaagac | acggccccc | ggaggatggg | tgatggaggg | 180 |
| agacaagctg | gtcctcatct | gctcgggttg | tagagtcaact | gggaatataa | cttacttctg | 240 |
| gtacagaggg | gccctggggt | tccaactgga | aacaaagaca | caaccttcac | taacagcaga | 300 |
| gtttgagatc | agtgacatga | agcagagcga | tgctgatcaa | tattactgtg | cggctaacga | 360 |
| tgccacagac | cctatcgcca | gtgagctggg | gagcatccac | gtcagagtcc | cagtgtctcg | 420 |
| ccctgtcctt | acgtttgggg | actctggaac | ccaggctgtg | ctaggggacc | tggtggagct | 480 |
| tactgttaag | gocctgagag | gctcaccctc | aattctctac | cagttttatc | atgagagcat | 540 |
| catcctgggg | aacagttcag | caccctcttg | aggaggagca | tccctcaact | tctccctgac | 600 |
| tgagaacat | tctggaaact | tctcctgtga | ggccagcaat | ggacaggggtg | cccaacgaag | 660 |
| tgaggtgggtg | gctctcaact | taacaggtct | ctccttagtg | cctactgaga | atggaatcag | 720 |
| ccatctctoc | ttaggactca | ctgggtggct | gcttggctgt | cttagcccca | tcaccatggc | 780 |

```

cttaatatattt tgctactggc tcaagagaaa aataggaaga cagtcagagg atccagtcag      840
gagccctcct cagactgtgc tccaaggatc cacgtacccc aaatcccccg actcaaggca      900
gccagagccc ctgtatgaga acgtgaacgt tgtaagtggc aatgaagtgt actctctggt      960
gtaccacacc ccgcaggtgc tggaaccagc agcagctcag catgtgagga cacacggagt     1020
aagtgaagtcc tttoagggtct cctctggact ctattctaag ccaaggataa acattgcaca     1080
tatggactat gaagacgcca tgtagaatta tgtaaacagc aactatggag tgctacatac     1140
aagcccaagg cctgatgtgg cctccaagga tactggggac agggatagct tgccagccca     1200
atctcccccac acactgogggt tcattagatg agtccttcac ctaccctgtg tgaagctgga     1260
gcaagtccctg cagaaaccac ccaggaaaaac caacttagac ggagaagcca gaagcatttg     1320
catctggttg ttgoccatto atgttggcac acgaactttt atttacagga ggaaaatggt     1380
gtgatgaaag caactaagggt cttacagcag agggacaatg cgactcagag agcacaagc     1440
cgagatcaat ggctttgcag gtctgtgtgt gagacagagc catgtctcct ctgtgcacat     1500
accctagagt acttotgagt cactgoccat aacttagaat taaacacagt tgcataaaat     1560
gtactgt

```

<210> 89

<211> 1032

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 89

```

atgtctacctt ggctcctgct actgatctgt gctctaccgt gtgaacctgc tggaatctct      60
gatgtgagct tgaagacacg gccccagga ggatgggtga tggagggaga caagctggtc     120
ctcatctgct cggttgatag agtcactggg aatataactt acttctggta cagaggggccc     180
ctgggtttcc aactggaaaac aaagacacaa ccttcaactaa cagcagagtt tgagatcagt     240
gacatgaagc agagcgatgc tgatcaatat tactgtgcgg ctaacgatgg ccacgacctt     300
atcgccagtg agctgggtgag catccacgtc agagttccag tgtctogccc tgtccttacg     360
tttggggact ctggaaccca ggctgtgcta ggggacctgg tggagcttca ctgtaaggcc     420
ctgagaggct ccccccaat cttctaccag ttttatcatg agagcatcat cctggggaac     480
agttcagcac cctctggagg aggagcatcc ttcaacttct cctgactgc agaacttct     540
ggaaactttt cctgtgaggc cagcaatgga cagggtgccc aacgaagtga ggtggtggct     600
ctcaacttaa caggctcttc cttagtgcct actgagaatg gaatcagcca tctctcctta     660
ggactcactg ggtggctgct tggctgtctt agcccatca ccatggcctt aatattttgc     720
tactggctca agagaaaaat aggaagacag tcagaggatc cagtcaggag ccttcctcag     780
actgtgctcc aaggatccac gtaccccaaa tcccccgact caaggcagcc agagccccctg     840
tatgagaacg tgaacgttgt aagtggcaat gaagtgtact ctctgggtga ccacaccccg     900
cagggtgctg aaccagcagc agctcagcat gtgaggacac acggagtaag tgagtctttt     960
caggctcctc ctggactota ttctaagcca aggataaaca ttgcacatat ggactatgaa     1020
gacgccatgt ag

```

<210> 90

<211> 981

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 90

```

ggaatctctg atgtgagctt gaagacacgg cccccaggag gatgggtgat ggagggagac      60
aagctgggtcc tcatctgctc ggttgataga gtcactggga atataactta cttctgggtac     120
agagggggccc tgggtttcca actggaaaca aagacacaaac cttcactaac agcagagttt     180
gagatcagtg acatgaagca gagcgatgct gatcaatatt actgtgcggc taacgatggc     240
cacgacccta togccagtga gctgggtgag atccacgtca gagttccagt gtctcgccct     300
gtccttaacgt ttggggactc tggaaccagc gctgtgctag gggacctggg ggagcttcac     360
tgtaaggccc tgagaggctc acccccaatc ttctaccagt tttatcatga gagcatcatc     420

```


| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| ctggggaaca | gttcagcacc | ctctggagga | ggagcatcct | tcaacttctc | cctgactgca | 480 |
| gaacattctg | gaaacttctc | ctgtgaggcc | agcaatggac | aggggtgccc | acgaagtgg | 540 |
| gtggtggctc | tcaacttaac | aggtctctcc | ttagtgccca | ctgagaatgg | aatcagccat | 600 |
| ctctccttag | gactcactgg | gtggctgctt | ggctgtctta | gccccatcac | catggcctta | 660 |
| atattttgct | actggctcaa | gagaaaaata | ggaagacagt | cagaggatcc | agtcaggagc | 720 |
| cctcctcaga | ctgtgctcca | aggatccacg | taccccaaat | cccccgactc | aaggcagcca | 780 |
| gagcccctgt | atgagaacgt | gaacgtttgt | agtggcaatg | aagtgtactc | tctgggtgtac | 840 |
| cacaccccg | aggtgctgga | accagcagca | gctcagcatg | tgaggacaca | cggagtaagt | 900 |
| gagtcctttc | aggtctcctc | tggactctat | tctaagccaa | ggataaacat | tgcacatatg | 960 |
| gactatgaag | acgccatgta | g | | | | 981 |

<210> 91

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 91

| | | | | | | |
|-------------|-------------|------------|------------|------------|-------------|-----|
| atgctacott | ggctcctgct | actgatctgt | gctctaccgt | gtgaacctgc | tggaatctct | 60 |
| gatgtgagct | tgaagacacg | gccccagga | ggatgggtga | tggagggaga | caagctggctc | 120 |
| ctcatctgct | cggttgatag | agtcactggg | aatataactt | acttctggta | cagagggggcc | 180 |
| ctgggtttcc | aactggaaac | aaagacacaa | ccttcactaa | cagcagagtt | tgagatcagt | 240 |
| gacatgaagc | agagcgatgc | tgatcaatat | tactgtgcgg | ctaacgatgg | ccacgacctc | 300 |
| atcgccagtg | agctgggtgag | catccacgtc | agagttccag | tgtctcgccc | tgtccttacg | 360 |
| tttgggggact | ctggaaccca | ggctgtgcta | ggggacctgg | tggagcttca | ctgtaaggcc | 420 |
| ctgagaggct | cacccccaat | cttctaccag | ttttatcatg | agagcatcat | cctggggaac | 480 |
| agttcagcac | cctctggagg | aggagcatcc | ttcaacttct | ccctgactgc | agaacattct | 540 |
| ggaaaacttct | cctgtgaggc | cagcaatgga | caggggtgcc | aacgaagtga | gggtgggtgct | 600 |
| ctcaacttaa | caggtctctc | cttagtgcct | actgagaatg | gaatcagcca | tctctcctta | 660 |

<210> 92

<211> 609

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 92

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| ggaatctctg | atgtgagctt | gaagacacgg | ccccaggag | gatgggtgat | ggaggggagac | 60 |
| aagctgggtcc | tcatctgctc | ggttgataga | gtcactggga | atataactta | cttctgggtac | 120 |
| agagggggccc | tgggtttcca | actggaaaca | aagacacaa | cttcactaac | agcagagtct | 180 |
| gagatcagtg | acatgaagca | gagcgatgct | gatcaatatt | actgtgcggc | taacgatggc | 240 |
| cacgacccta | tcgccagtga | gctggtgagc | atccacgtca | gagttccagt | gtctcgccct | 300 |
| gtccttacgt | ttggggactc | tggaaaccag | gctgtgctag | gggacctggg | ggagcttcac | 360 |
| tgtgaaggccc | tgagaggctc | acccccaatc | ttctaccagt | tttatcatga | gagcatcatc | 420 |
| ctggggaaca | gttcagcacc | ctctggagga | ggagcatcct | tcaacttctc | cctgactgca | 480 |
| gaacattctg | gaaacttctc | ctgtgaggcc | agcaatggac | aggggtgccc | acgaagtgg | 540 |
| gtggtggctc | tcaacttaac | aggtctctcc | ttagtgccca | ctgagaatgg | aatcagccat | 600 |
| ctctcctta | | | | | | 609 |

<210> 93

<211> 303

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 93
aagagaaaaa taggaagaca gtcagaggat ccagtcagga gccctcctca gactgtgctc 60
caaggatcca cgtaccccaa atccccgac tcaaggcagc cagagcccct gtatgagaac 120
gtgaacgttg taagtggcaa tgaagtgtac tctctggtgt accacacccc gcagggtgctg 180
gaaccagcag cagctcagca tgtgaggaca caggagtaa gtgagtcctt tcagggtctcc 240
tctggactct attctaagcc aaggataaac attgcacata tggactatga agacgccatg 300
tag 303

<210> 94

<211> 1567

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 94
tgagtagtct ggttttgctt ttttttcttt tggtagagagg taccttcaag ttaccatccc 60
cagcctgggt ctcattgctac cttggctcct gctactgato tgtgctctac cgtgtgaacc 120
tgctggaaac tctgatgtga gcttgaagac acggcccccga ggaggatggg tgatggaggg 180
agacaagctg gtccctcatct gctcgggttg tagagtcact gggaaatataa cttacttctg 240
gtacagaggg gccctgggtt tccaactgga aacaaagaca caaccttcac taacagcaga 300
gtttgagatc agtgacatga agcagagcga tgctgatcaa tattactgtg cggctaacga 360
tggccacgac cctatcgcca gtgagctggt gagcatccac gtcagagttc cagtgtctcg 420
ccctgtcctt acgtttgggg actctggaac ccaggctgtg ctagggggacc tggtagagct 480
tcaactgtaag gccctgagag gctcaccccc aatcttctac cagttttatc atgagagcat 540
catcctgggg aacagttcag caccctctgg aggaggagca tccttcaact tctccctgac 600
tgcagaacat tctggaaact tctcctgtga ggccagcaat ggacaggggtg cccaacgaag 660
tgagggtggt gctctcaact taacaggctc ctccttagtg cctactgaga atggaatcag 720
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gagccctcct cagactgtgc tccaaggatc cagctacccc aaatcccccg actcaaggca 900
gccagagccc ctgtatgaga acgtgaacgt tgtaagtggc aatgaagtgt actctctggt 960
gtaccacacc ccgaggtgac tggaaaccagc agcagctcag catgtgagga cacacggagt 1020
aagtgagtc tttcaggtct cctctggact ctattctaag ccaaggataa acattgcaca 1080
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aagcccaagg cctgatgtgg cctccaagga tactggggac agggatagct tgccagccca 1200
atttcccac acactgcgtt tcattagatg agtccctcac ctaccctgtg tgaagctgga 1260
gcaagtcctg cagaaaccac ccaggaaaac caacttagac ggagaagcca gaagcatttg 1320
catctgggtt ttgcccattc atgttggcac acgaactttt atttacagga ggaaaatggt 1380
gtgatgaaag caactaaggc cttacagcag agggacaatg cgactcagag agcacaagc 1440
cgagatcaat ggctttgcag gtctgctgtg gagacagagc catgcttcct ctgtgcacat 1500
accctagagt acttctgagt cactgccatc aacttagaat taaacacagt tgcataaaat 1560
gtactgt 1567

<210> 95

<211> 903

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 95
atgctacctt ggctcctgct actgatctgt gctctaccgt gtgaacctgc tggaaatctct 60
gatgtgagct tgaagacacg gccccagga ggatgggtga tggagggaga caagctggtc 120

```

ctcatctgct cggttgatag agtcactggg aatataactt acttctggta cagagggggcc 180
ctgggtttcc aactggaaac aaagacacaa ctttacttaa cagcagagtt tgagatcagt 240
gacatgaagc agagcgatgc tgatcaatat tactgtgcgg ctaacgatgg ccacgacct 300
atcgccagtg agctgggtgag catccacgto agagttccag tgtctcgccc tgtccttacg 360
tttggggact ctggaaacca ggctgtgcta ggggacctgg tggagcttca ctgtaaggcc 420
ctgagaggct caccocccaat cttctaccag ttttatcatg agagcatcat cctgggggaa 480
agttcagcac cctctggagg aggagcatoc ttcaacttct ccctgactgc agaacattct 540
ggaaacttct cctgtgaggc cagcaatgga caggggtgccc aacgaagtga ggtgggtggc 600
ctcaacttaa caggaagaca gtcagaggat ccagtcagga gccctcctca gactgtgctc 660
caaggatcca cgtaccccaa atcccccgac tcaaggcagc cagagccccct gtatgagaac 720
gtgaacgttg taagtggcaa tgaagtgtac tctctggtgt accacacccc gcaggtgctg 780
gaaccagcag cagctcagca tgtgaggaca caggagtaa gtgagtcctt tcaggtctcc 840
tctggactct attctaagcc aaggataaac attgcacata tggactatga agacgccatg 900
tag 903

```

<210> 96

<211> 852

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 96

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ggaatctctg atgtgagctt gaagacacgg cccccaggag gatgggtgat ggagggagac 60
aagctgggtc tcatctgctc ggttgataga gtcactggga atataactta cttctgggtac 120
agagggggccc tgggtttcca actggaaaca aagacacaa cttcactaac agcagagttt 180
gagatcagtg acatgaagca gagcgatgct gatcaatatt actgtgcggc taacgatggc 240
cacgacccta tcgocagtg gctgggtgagc atccacgtca gagttccagt gtctcgccct 300
gtccttacgt ttggggactc tggaaaccag gctgtgctag gggacctggg ggagcttcac 360
tgtaaggccc tgagaggctc acccccaatc ttctaccagt tttatcatga gagcatcatc 420
ctggggaaca gttcagcacc ctctggagga ggagcatcct tcaacttctc cctgactgca 480
gaacattctg gaaacttctc ctgtgaggcc agcaatggac agggtgccca acgaagtga 540
gtgggtggctc tcaacttaac aggaagacag tcagaggatc cagtcaggag ccctcctcag 600
actgtgctcc aaggatccac gtaccccaaa tcccccgact caaggcagcc agagccccctg 660
tatgagaacg tgaacgttgt aagtggcaat gaagtgtact ctctggtgta ccacaccccg 720
caggtgctgg aaccagcagc agctcagcat gtgaggacac acggagtaag tgagtccttt 780
caggtctcct ctggactcta ttctaagcca aggataaaca ttgcacatat ggactatgaa 840
gacgccatgt ag 852

```

<210> 97

<211> 2447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 97

```

attcaagtta cactcaactg ttttagaaga gcagttcccc agatttctcc ttggagctgt 60
gagtgactac cattgcgagc aagagcaaga ggaaagcact acctgtgagc agatgtctgg 120
ttcattctoa ccctgtgtgg tgttcacaca gatgtggctg actctactgg ttgtgactcc 180
tgtcaatgga cagcatgaag ctgcacagca gtctgtgggt tcccttcagc ctccatggac 240
cactttcttt cgaggagagg tcgtcacact gacttggtat agattcggct tctccgtacc 300
ccagaaaaca aaatggtacc agaaaagaaa aacagtgaag caaaccocag gtgcttttgg 360
aattaaagca cataccttaa aggtccatga gtccggagag tattggtgoc aagccgacag 420
cttacttccg agcatgcacg tgaacgtaga gttttctgaa gattttctgg tgctgcaagc 480
tccacctgct gtgtttgaag gagactctgt ggttctgagg tgctacgcaa agaaaggcat 540
agaagcagag accctgacat tttacaagga tggtaaagct ctgacattac atcatcaaag 600

```

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|------|
| tgagctctct | attcatcatg | caaactctgaa | ggacaacggg | caatacaaat | gcacttcgaa | 660 |
| gaagaagtgg | tcttttgggt | ccctctatac | ttccaatacg | gtcggagttc | aagtccaaga | 720 |
| gttggtccca | cggtctgtgc | tgagagccag | accctcccat | cccatagatg | gaagtccagt | 780 |
| gaccctgacg | tgtcagaccc | agctctctgc | acagaagtca | gatgcccggc | tccagttctg | 840 |
| tttcttcaga | aacctccagc | ttctggggtc | aggctgcagc | cgctcctcag | agtttcacat | 900 |
| tcctgccata | tggactgaag | agtcaaggag | ataccagtgc | aaggcagaaa | cagtgaattc | 960 |
| ccaagttaga | aaacaaagta | cagcgttcat | aatcccagtg | cagagagctt | ctgcgagatt | 1020 |
| ccaaacacac | atcatcccag | cctcaaagtt | ggtgtttgaa | gggcagttgc | tgttactcaa | 1080 |
| ctgctcagta | aaaggagtyc | caggrrccct | caaattctcc | tggtataaaa | aggacatgct | 1140 |
| gaatgaagaa | acaaagattc | ttaagtccct | caacgcagaa | ttcaagatct | cccaggtgaa | 1200 |
| catcagtgc | gcaggggagt | atcactgtga | agctaccaac | agccgccgaa | gctttgtcag | 1260 |
| cagggcattt | cccatcacca | taaaagtccc | agtatctcaa | ccagttctca | ccctaagcac | 1320 |
| aggcaagacc | caggcccttg | agggagactt | gatgacactt | cattgtcaat | cccagagggg | 1380 |
| ctctccatgt | atcctgtatg | aattcttcta | tgagaatgtc | tccctgggga | atagctctat | 1440 |
| actctctgga | ggaggagcat | acttcaattt | ctctatgagc | acagagcgat | ctggaaacta | 1500 |
| ctactgcaca | gcagacaatg | gcctggggagc | ccagtgcagt | gaagctataa | ggatctctat | 1560 |
| ctttgacatg | acaaagaaca | gaagtgttcc | tatggctgcc | ggaatcactg | tgggactgct | 1620 |
| catcatggct | gttggagtgt | ttctgtttta | ttgctgggtc | tctagaaaag | caggaggaaa | 1680 |
| gcctacctct | gatgactcca | gaaacccttc | agattcagaa | ccccaggagc | ccacctatta | 1740 |
| caacgtacca | gcctgtatag | aactgcagcc | agtgtacagc | aatgagcctg | aggaaaacgt | 1800 |
| gatttacaca | gaagtacgga | gaactcaacc | aagacagaaa | catgcagatc | aggagtctga | 1860 |
| aagcccaaga | tcaaggtgcc | agatggctga | gaaaaagtag | gatatgtctc | ctccaagaac | 1920 |
| agctccagaa | aagaaacccg | aagcttcgtc | agtctaattc | caccgatgct | tctactgggc | 1980 |
| ctgcactttc | ctaccacagg | atggctccac | agatcatgga | cagcaaggaa | atggccaact | 2040 |
| ctcctaagac | tgggccaaca | tccccatctt | ctctttgggt | tcccagagcc | acgccacccc | 2100 |
| aaagtcagca | ggaagttgca | aaagatcaca | acgaccctat | tcctgttttg | taaccacccc | 2160 |
| cagcctgaag | caggctgagc | cagaccttga | ccttgtgtgc | actaaggaga | ttacctaggg | 2220 |
| tggagcctgc | ctctctagat | cactctattg | ttcagccact | gccactgttc | tccttcaaga | 2280 |
| cactgctacc | tgctggggag | ccactgagct | attccagaga | ctacacccta | tcctgcacat | 2340 |
| catcacctgt | agcctgttcc | aggctccaag | aatgaattgg | cggcaatggg | cctccccctt | 2400 |
| acccccctta | taagtgcatt | tgccattaaa | catttgggct | ttgatct | | 2447 |

<210> 98

<211> 1788

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 98

| | | | | | | |
|-------------|------------|-------------|------------|-------------|-------------|------|
| atgtctgggt | cattctcacc | ctgtgtgggtg | ttcacacaga | tgtggctgac | tctactgggt | 60 |
| gtgactcctg | tcaatggaca | gcatgaagct | gcacagcagt | ctgtgggttc | ccttcagcct | 120 |
| ccatggacca | ctttctttcg | aggagaggto | gtcacactga | cttggttatag | attcggcttc | 180 |
| tccgtacccc | agaaaacaaa | atggtaccag | aaaagaaaaa | cagtgaagca | aaccccaggt | 240 |
| gctttggtta | ttaaagcaca | taccttaaag | gtccatgagt | ccggagagta | ttggtgccaa | 300 |
| gccgacagct | tacttccgag | catgcacgtg | aacgtagagt | tttctgaaga | ttttctgggtg | 360 |
| ctgcaagctc | cacctgctgt | gtttgaagga | gactctgttg | ttctgagggtg | ctacgcaaaag | 420 |
| aaaggcatag | aagcagagac | cctgacattt | tacaaggatg | gtaaagctct | gacattacat | 480 |
| catcaaagtg | agctctctat | tcatcatgca | aatctgaagg | acaacgggtca | atacaaatgc | 540 |
| acttccaaga | agaagtggtc | ttttgggtcc | ctctataact | ccaatacggg | cggagttcaa | 600 |
| gtccaagagt | tgttcccacg | gcctgtgctg | agagccagac | cctcccatcc | catagatgga | 660 |
| agtccagtga | ccctgacgtg | tcagaccag | ctctctgcac | agaagtcaga | tgcccggctc | 720 |
| cagttctgtt | tcttcagaaa | cctccagctt | ctgggggcag | gotgcagccg | ctcctcagag | 780 |
| tttcacattc | ctgccatag | gactgaagag | tcaaggagat | accagtgcaa | ggcagaaaca | 840 |
| gtgaattccc | aagttagaaa | acaaagtaca | gcgttcataa | tcccagtgca | gagagcttct | 900 |
| gogagattcc | aaacacacat | catcccagcc | tcaaagttgg | tgtttgaaag | gcagttgctg | 960 |
| ttactcaact | gtcagtaaa | aggagtycca | ggrccctca | aattctcctg | gtataaaaaag | 1020 |
| gacatctga | atgaagaaac | aaagattctt | aagtcctcca | acgcagaatt | caagatctcc | 1080 |
| cagggtgaaca | tcagtgcagc | aggggagtat | cactgtgaag | ctaccaacag | ccgccgaagc | 1140 |

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|------|
| tttgtcagca | gggcatttcc | catcaccata | aaagtcccag | tatctcaacc | agttctcacc | 1200 |
| ctaagcacag | gcaagaccca | ggcccttgag | ggagacttga | tgacacttca | ttgtcaatcc | 1260 |
| cagaggggct | ctccatgtat | cctgtatgaa | ttcttctatg | agaatgtctc | cctggggaat | 1320 |
| agctctatac | tctctggagg | aggagcatac | ttcaatttct | ctatgagcac | agagcgatct | 1380 |
| ggaaactact | actgcacagc | agacaatggc | ctggggagccc | agtgcagtga | agctataagg | 1440 |
| atctctatct | ttgacatgac | aaagaacaga | agtgttccta | tggctgccgg | aatcactgtg | 1500 |
| ggactgctca | tcatggctgt | tggagtgttt | ctgttttatt | gctggttctc | tagaaaagca | 1560 |
| ggaggaaagc | ctacctctga | tgactccaga | aacccttcag | attcagaacc | ccaggagccc | 1620 |
| acctattaca | acgtaccagc | ctgtatagaa | ctgcagccag | tgtacagcaa | tgagcctgag | 1680 |
| gaaaacgtga | tttacacaga | agtacggaga | actcaaccaa | gacagaaaca | tgcagatcag | 1740 |
| gagtctgaaa | gcccaagatc | aaggtgccag | atggctgaga | aaaagtag | | 1788 |

<210> 99

<211> 1710

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 99

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|------|
| cagcatgaag | ctgcacagca | gtctgtggtt | tcccttcagc | ctccatggac | cactttcttt | 60 |
| cgaggagagg | tcgtcacact | gacttggtat | agattcggtt | tctccgtacc | ccagaaaaca | 120 |
| aaatggtaac | agaaaagaaa | aacagtgaag | caaaccacag | gtgctttggt | aattaaagca | 180 |
| cataccttaa | aggtccatga | gtccggagag | tattggtgcc | aagccgacag | cttacttccg | 240 |
| agcatgcacg | tgaacgtaga | gttttctgaa | gattttctgg | tgctgcaagc | tccacctgct | 300 |
| gtgtttgaag | gagactctgt | ggttctgagg | tgctacgcaa | agaaaggcat | agaagcagag | 360 |
| accctgacat | tttacaagga | tggtaaaagt | ctgacattac | atcatcaaag | tgagctctct | 420 |
| attcatcatg | caaactctga | ggacaacggt | caatacaaat | gcacttcgaa | gaagaagtgg | 480 |
| tcttttgggt | ccctctatac | ttccaatacg | gtcggagtgc | aagtccaaga | gttgttccca | 540 |
| cggcctgtgc | tgagagccag | accctcccat | cccatagatg | gaagtccagt | gaccctgacg | 600 |
| tgtcagaccc | agctctctgc | acagaagtca | gatgcccggc | tccagttctg | tttcttcaga | 660 |
| aacctccagc | ttctgggggc | aggctgcagc | cgctcctcag | agtttcacat | tcctgccata | 720 |
| tggactgaag | agtcaaggag | ataccagtgc | aaggcagaaa | cagtgaattc | ccaagttaga | 780 |
| aaacaaaagta | cagcgttcat | aatcccagtg | cagagagctt | ctgcgagatt | ccaaacacac | 840 |
| atcatcccag | cctcaaagtt | ggtgtttgaa | gggcagttgc | tgttactcaa | ctgctcagta | 900 |
| aaaggagtyc | caggrccctt | caaattctcc | tggtataaaa | aggacatgct | gaatgaagaa | 960 |
| acaaagattc | ttaagtcctc | caacgcagaa | ttcaagatct | cccaggtgaa | catcagtgc | 1020 |
| gcaggggagt | atcactgtga | agctaccaac | agccgcccga | gctttgtcag | cagggcattt | 1080 |
| cccatacaca | taaaagtccc | agtatctcaa | ccagttctca | ccctaagcac | aggcaagacc | 1140 |
| caggcccttg | aggagactt | gatgacactt | cattgtcaat | cccagagggg | ctctccatgt | 1200 |
| atcctgtatg | aattcttcta | tgagaatgtc | tccctgggga | atagctctat | actctctgga | 1260 |
| ggaggagcat | acttcaattt | ctctatgagc | acagagcgat | ctggaaacta | ctactgcaca | 1320 |
| gcagacaatg | gcctgggagc | ccagtgcagt | gaagctataa | ggatctctat | ctttgacatg | 1380 |
| acaaagaaca | gaagtgttcc | tatggctgcc | ggaatcactg | tgggactgct | catcatggct | 1440 |
| gttggagtgt | ttctgtttta | ttgctggttc | tctagaaaag | caggaggaaa | gcctacctct | 1500 |
| gatgactoca | gaaacccttc | agattcagaa | ccccaggagc | ccacctatta | caacgtacca | 1560 |
| gcctgtatag | aactgcagcc | agtgtacagc | aatgagcctg | aggaaaacgt | gatttacaca | 1620 |
| gaagtacgga | gaactcaacc | aagacagaaa | catgcagatc | aggagtctga | aagcccaaga | 1680 |
| tcaaggtgcc | agatggctga | gaaaaagtag | | | | 1710 |

<210> 100

<211> 1401

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

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<400> 100
cagcatgaag ctgcacagca gtctgtggtt tcccttcagc ctccatggac cactttcttt 60
cgaggagagg tcgtcacact gacttggtat agattcggct tctcogtacc ccagaaaaca 120
aaatggtacc agaaaagaaa aacagtgaag caaaccacag gtgctttggt aattaaagca 180
cataccttaa aggtccatga gtccggagag tattggtgcc aagccgacag cttacttccg 240
agcatgcaag tgaacgtaga gttttctgaa gattttctgg tgctgcaagc tccacctgct 300
gtgtttgaag gagactctgt ggttctgagg tgctacgcaa agaaaggcat agaagcagag 360
accctgacat tttaacaagga tggtaaagct ctgacattac atcatcaaag tgagctctct 420
attcatcatg caaatctgaa ggacaacggg caatacaaat gcacttcgaa gaagaagtgg 480
tcttttgggt cctctataac ttccaatacg gtccgagttc aagtccaaga gttgttccca 540
cggcctgtgc tgagagccag accctcccat cccatagatg gaagtccagt gaccctgacg 600
tgtcagaccc agctctctgc acagaagtca gatgccgggc tccagttctg tttcttcaga 660
aacctccagc ttctgggggtc aggctgcagc cgctcctcag agtttcacat toctgccata 720
tggactgaag agtcaaggag ataccagtgc aaggcagaaa cagtgaattc ccaagttaga 780
aaacaaagta cagcgttcat aatcccagtg cagagagctt ctgcgagatt ccaaacacac 840
atcatccag cctcaaagtt ggtgtttgaa gggcagttgc tgttactcaa ctgctcagta 900
aaaggagtyc caggrcccct caaattctcc tggataaaaa aggacatgct gaatgaagaa 960
acaaagattc ttaagtccct caacgcagaa ttcaagatct cccaggtgaa catcagtgac 1020
gcaggggagt atcactgtga agctaccaac agccgccgaa gctttgtcag cagggcattt 1080
cccattacca taaaagtccc agtatctcaa ccagttctca cctaagcac aggcaagacc 1140
caggcccttg agggagactt gatgacactt cattgtcaat cccagagggg ctctccatgt 1200
atcctgtatg aattcttcta tgagaatgtc tccctgggga acagagcgat ctggaacta ctactgcaca 1260
ggaggagcat acttcaattt ctctatgagc ctgagcgat ctggaacta ctactgcaca 1320
gcagacaatg gcctgggagc ccagtgcagt gaagctataa ggatctctat ctttgacatg 1380
acaaagaaca gaagtgttcc t 1401

```

<210> 101

<211> 1479

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

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<400> 101
atgtctgggtt cattctcacc ctgtgtgggtt ttcacacaga tgtggctgac tctactgggtt 60
gtgactcctg tcaatggaca gcatgaagct gcacagcagt ctgtgggtttc ccttcagcct 120
ccatggacca ctttcttttg aggagaggct gtcacactga cttgttatag attcggcttc 180
tccgtacccc agaaaacaaa atggtaccag aaaagaaaaa cagtgaagca aaccccagg 240
gctttggtaa ttaaagcaca taccttaaaag gtccatgagt cgggagagta ttgggtgcaa 300
gccgacagct tacttccgag catgcacgtg aacgtagagt tttctgaaga ttttctgggtg 360
ctgcaagctc cacctgctgt gtttgaagga gactctgtgg ttctgagggtg ctacgcaaag 420
aaaggcatag aagcagagac cctgacattt tacaaggatg gtaaaagctct gacattacat 480
catcaaagtg agctctctat tcatcatgca aatctgaagg acaacgggtc atacaaatgc 540
acttcgaaga agaagtggtc ttttgggtcc ctctatactt ccaatacggg cggagttcaa 600
gtccaagagt tgttcccacg gcctgtgctg agagccagac cctcccatcc catagatgga 660
agtccagtga ccctgacgtg tcagaccag ctctctgcac agaagtcaga tgcccggctc 720
cagttctggt tcttcagaaa cctccagctt ctgggggtcag gctgcagccg ctccctcagag 780
tttcacattc ctgccatag gactgaagag tcaaggagat accagtgcaa ggcagaaaaca 840
gtgaattccc aagttagaaa acaaagtaca gcgttcataa tcccagtgca gagagcttct 900
gcgagattcc aaacacacat catcccagcc tcaaagttgg tgtttgaagg gcagttgctg 960
ttactcaact gctcagtaaa aggagtycca ggroccctca aattctcctg gtataaaaag 1020
gacatgctga atgaagaaac aaagattctt aagtcctcca acgcagaatt caagatctcc 1080
caggtgaaca tcagtgcgc aggggagtat cactgtgaag ctaccaacag ccgccgaagc 1140
tttgtcagca gggcatttcc catcaccata aaagtcccag tatctcaacc agttctcacc 1200
ctaagcacag gcaagaccca ggcccttgag ggagacttga tgacacttca ttgtcaatcc 1260
cagaggggct ctccatgtat cctgtatgaa ttcttctatg agaatgtctc cctggggaat 1320
agctctatac tctctggagg aggagcatac ttcaatttct ctatgagcac agagcgatct 1380
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<210> 102

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
synthetic construct

<400> 102

| | | | | | | |
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| ccccaggagc | ccacctatta | caacgtacca | gcctgtatag | aactgcagcc | agtgtacagc | 120 |
| aatgagcctg | aggaaaacgt | gatttacaca | gaagtacgga | gaactcaacc | aagacagaaa | 180 |
| catgcagatc | aggagtctga | aagcccaaga | tcaagggtgcc | agatggctga | gaaaaagtag | 240 |